

*check hit 10
mur leu 3a*

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OM protein - protein search, using SW model

Run on: February 14, 2003, 11:04:17 ; Search time 13.5484 Seconds
(without alignments)
49.176 Million cell updates/sec

Title: US-09-701-001b-1
Perfect score: 27
Sequence: 1 DYVIN 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database:

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- 9: /SID2/gcgcdata/geneseq/geneseq-emb1/AA1988.DAT:*
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- 11: /SID2/gcgcdata/geneseq/geneseq-emb1/AA1990.DAT:*
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- 21: /SID2/gcgcdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SID2/gcgcdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID2/gcgcdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	100.0	5	21	AAV59256	Antibody 4H5 H cha
2	27	100.0	5	21	AAV51133	Murine CD4/CD34 re
3	27	100.0	61	23	ABP07152	Human ORFX protein
4	27	100.0	110	21	AAV59262	Antibody 4H5 H cha
5	27	100.0	110	21	AAV51139	Murine derived pro
6	27	100.0	113	22	ABP71922	Drosophila melanog
7	27	100.0	118	21	AAV59266	Antibody 4H5 H cha
8	27	100.0	118	21	AAV51143	Murine derived pro
9	27	100.0	118	21	AAV51145	Murine derived pro
10	27	100.0	122	11	AAV04135	Anti-Leu 3a heavy

11	27	100.0	131	22	AAV64639	Human secreted pro
12	27	100.0	136	11	AAV04133	Anti-Leu 3a heavy
13	27	100.0	149	22	ABP68170	Drosophila melanog
14	27	100.0	303	23	ABP54572	Lactococcus lactis
15	27	100.0	305	21	AAV59264	Antibody 4H5 H cha
16	27	100.0	305	21	AAV59265	Antibody 4H5 L cha
17	27	100.0	305	21	AAV51141	Murine derived pro
18	27	100.0	305	21	AAV51142	Murine derived pro
19	27	100.0	348	21	AAV82330	Pyrococcus horikosi
20	27	100.0	348	21	AAV82330	Pyrococcus horikosi
21	27	100.0	366	18	AAV6816	Putative P. abyssi
22	27	100.0	399	21	AAV40248	B. cereus leuDH pr
23	27	100.0	444	23	ABP43940	Human cancer assoc
24	27	100.0	507	20	ABP29082	Streptococcus poly
25	27	100.0	543	22	AAV34756	C. pneumoniae prot
26	27	100.0	616	22	ABP63767	Drosophila melanog
27	27	100.0	722	22	ABP56000	Escherichia coli p
28	27	100.0	778	22	ABP52838	Drosophila melanog
29	27	100.0	933	19	AAV98599	H. pylori GHPD 127
30	27	100.0	990	23	ABP09640	MutB protein of th
31	26	96.3	97	22	AAV03560	Human glycosyl-pho
32	26	96.3	99	23	ABP04400	Human polyphosphat
33	26	96.3	102	22	AAV03006	Myobacterium spec
34	26	96.3	113	20	AAV04864	Arabidopsis thalia
35	26	96.3	122	21	AAV56333	Myobacterium spec
36	26	96.3	127	20	AAV04862	Enterococcus faeca
37	26	96.3	139	22	AAV35109	Arabidopsis thalia
38	26	96.3	146	21	AAV56333	Arabidopsis thalia
39	26	96.3	157	21	AAV55873	S. epidermidis ope
40	26	96.3	182	22	AAV82660	S. epidermidis ope
41	26	96.3	215	21	AAV83015	Amilno acid sequenc
42	26	96.3	214	22	AAV07844	Human AE001086 sar
43	26	96.3	223	22	AAV08083	Staphylococcus epi
44	26	96.3	233	23	ABP39000	Human ORFX ORF1469
45	26	96.3	249	21	AAV41705	

ALIGNMENTS

RESULT 1
AAV59256
AAV59256 standard; peptide: 5 AA.
ID
XX AAV59256;
AC
XX
XX
DT 17-APR-2000 (first entry)
DE Antibody 4H5 H chain variable region CDR1 fragment.
XX
XX CD4 antigen; anti-human; antibody; 4H5; drug; CDR;
KW complementarity determining region.
KM
XX
XX Mus sp.
OS
XX
XX JPI1332563-A.
PN
XX
XX 07-DEC-1999.
PD
XX
XX 26-MAY-1998; 98JP-0163034.
PF
XX
XX 26-MAY-1998; 98JP-0163034.
PR
XX
XX 26-MAY-1998; 98JP-0163034.
PS
XX (ASAH) ASAH KASEI KOGYO KK.
PA
XX WPI: 2000-091351/08.
DR
XX
XX An antibody and the nucleic acid coding the antibody -
PT
XX
XX Claim 1; Page 14; 25pp; Japanese.
PS
XX The invention provides an antibody having affinity to CD4 antigen. The
XX anti-human CD4 antibody 4H5 is used for the detection of antigen and
CC

CC application for drugs. It is highly safe in human dose. Sequences
CC AAY59256-58 represent the complementarity determining region (CDR)-1,
CC CDR-2 and CDR-3 fragments in the H chain variable region of the
CC antibody 4H5 respectively.
XX

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYVIN 5
DB 1 DYVIN 5

RESULT 2
AAY51133
ID AAY51133 standard; Protein; 5 AA.

XX AAY51133;

XX 31-MAR-2000 (first entry)

DE Murine CD4/CD34 recognizing antibody heavy chain CDR-1 region #1.

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
XX hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
XX HIV infection; autoimmune disease; complementarity determining region;
XX CDR-1; heavy chain; murine.

XX Mus sp.

XX WO9961629-A1

XX 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711.

XX 25-MAY-1998; 98JP-0159957.

XX 26-MAY-1998; 98JP-0163023.

XX (ASAH) ASAH KASEI KOGYO KK.

XX (ASAH) ASAH MEDICAL CO LTD.

XX Ono M, Soka T, Morimoto I, Miyamura K;

XX WPI: 2000-086720/07.

XX Devices containing antibodies recognising CD4 or CD34 and their use for
XX the separation of CD4 or CD34 positive cells

XX Claim 3; Page 75; 11pp; Japanese.

XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for
XX the collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal
XX compositions for the treatment of HIV infection and autoimmune diseases.
XX This sequence represents a murine derived complementarity determining
XX region CDR-1 protein fragment which is used to illustrate the method of
XX the invention.

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 21; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYVIN 5

DB 1 DYVIN 5

RESULT 3
ABP07152
ID ABP07152 standard; Protein; 61 AA.

XX ABP07152;

XX 25-JUN-2002 (first entry)

XX Human ORFX protein sequence SEQ ID NO:14286.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
XX hyperproliferative disorder; psoriasis; benign tumor; haemorrhage;
XX degenerative disorder; osteoarthritis; neurodegenerative disorder;
XX cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
XX hypertension; hypothyroidism; cholesterol ester storage disease;
XX immune deficiency; immune disorder; infectious disease;
XX autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
XX myasthenia gravis.

XX Homo sapiens.

XX WO200192523-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US10836.

XX 30-MAY-2000; 2000US-206132P.

XX 29-AUG-2000; 2000US-228716P.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

XX WPI: 2002-106308/14.

XX N-PSDB; ABN22904.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
XX preventing and treating cardiovascular disease, neurodegenerative,
XX hyperproliferative disorders and autoimmune disorders

XX Disclosure; SEQ ID 14286; 1037pp; English.

XX The present invention describes substantially purified human proteins
XX (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
XX in the specification). ABN15762 to ABN27252 encode the human ORFX
XX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
XX treating or preventing a pathology associated with an ORFX-associated
XX disorder in humans, and in the manufacture of a medicament for treating a
XX syndrome associated with ORFX-associated disorder. ORFX polynucleotide
XX sequences can be used in gene therapy. ORFX sequences can be used in the
XX treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
XX psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,
XX osteoarthritis, neurodegenerative disorders, disorders related to organ
XX transplantation, cardiovascular diseases, diabetes mellitus, systemic
XX lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
XX storage disease, various immune deficiencies and disorders, infectious
XX diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
XX arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
XX disease and autoimmune inflammatory eye disease. ORFX proteins are also
XX useful for treating burns, incisions, ulcers, for treating osteoporosis,
XX bone degenerative disorders, or periodontal disease, and for gut
XX protection or regeneration and treatment of lung or liver fibrosis,
XX reperfusion injury in various tissues and conditions resulting from
XX systemic cytokine damage.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

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SQ Sequence 61 AA;
 Query Match 100.0%; Score 27; DB 23; Length 61;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYVIN 5
 DB 24 DYVIN 28
 RESULT 4
 AAY59262
 ID AAY59262 standard; protein; 110 AA.
 AC AAY59262;
 XX 17-APR-2000 (first entry)
 XX Antibody 4H5 H chain variable region.
 XX CD4 antigen; anti-human; antibody; 4H5; drug.
 XX Mus sp.
 XX JP11332563-A.
 XX 07-DEC-1999.
 XX 26-MAY-1998; 98JP-0163034.
 XX 26-MAY-1998; 98JP-0163034.
 XX (ASAH) ASAHI KASEI KOGYO KK.
 XX WPI; 2000-091351/08.
 XX N-PSDB; AAZ58661.
 XX An antibody and the nucleic acid coding the antibody -
 XX Claim 5; Page 15; 25pp; Japanese.
 XX The invention provides an antibody having affinity to CD4 antigen. The
 XX anti-human CD4 antibody 4H5 is used for the detection of antigen and
 XX application for drugs. It is highly safe in human dose. The present
 XX sequence represents the H chain variable region of the antibody 4H5.
 XX Sequence 110 AA;
 Query Match 100.0%; Score 27; DB 21; Length 110;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYVIN 5
 DB 23 DYVIN 27
 RESULT 5
 AAY51139
 ID AAY51139 standard; protein; 110 AA.
 AC AAY51139;
 XX 31-MAR-2000 (first entry)
 XX Murine derived protein fragment #1.
 XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 XX hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 XX HIV infection; autoimmune disease; murine.
 XX Mus sp.

XX WO9961629-A1.
 PN 02-DEC-1999.
 XX 24-MAY-1999; 99WO-JP02711. *int POT purify*
 XX 25-MAY-1998; 98JP-0159957.
 PR 26-MAY-1998; 98JP-0163023.
 XX (ASAH) ASAHI KASEI KOGYO KK.
 PA (ASAH) ASAHI MEDICAL CO LTD.
 XX Ono M, Soka T, Morimoto I, Miyamura K;
 PI WPI; 2000-086720/07.
 XX N-PSDB; AAZ44203.
 DR Devices containing antibodies recognising CD4 or CD34 and their use for
 XX the separation of CD4 or CD34 positive cells -
 PT Claim 22; Page 78; 111pp; Japanese.
 XX This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 XX SQ Sequence 110 AA;
 Query Match 100.0%; Score 27; DB 21; Length 110;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYVIN 5
 DB 23 DYVIN 27
 RESULT 6
 ABB71922
 ID ABB71922 standard; protein; 113 AA.
 XX AC ABB71922;
 XX 26-MAR-2002 (first entry)
 DT Drosophila melanogaster polypeptide SEQ ID NO 42558.
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 KW Drosophila melanogaster.
 XX OS WO200171042-A2.
 XX 27-SEP-2001.
 PD 23-MAR-2001; 2001WO-US09231.
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 BR (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX

DR WPI; 2001-656860/75.
 XX N-PSDB; ABL16025.
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 42558; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

Sequence 113 AA;

Query Match 100.0%; Score 27; DB 22; Length 113;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||||
 Db 54 DYVIN 58

RESULT 7
 AAY59266
 ID AAY59266 standard; protein; 118 AA.
 XX
 AC AAY59266;

17-APR-2000 (first entry)
 Antibody 4H5 H chain fragment.
 DE
 XX
 XX CD4 antigen; anti-human; antibody; 4H5; drug.
 XX

Mus sp.
 XX
 XX JP11332563-A.
 XX
 XX 07-DEC-1999.
 XX
 XX 26-MAY-1998; 98JP-0163034.
 XX
 XX 26-MAY-1998; 98JP-0163034.
 XX
 XX (ASAH) ASahi KASEI KOGYO KK.
 XX

WPI; 2000-091351/08.
 DR N-PSDB; AAY58689.
 XX

An antibody and the nucleic acid coding the antibody -
 PS Disclosure; Page 22; 25pp; Japanese.
 XX

CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents a H chain fragment of the antibody 4H5.
 XX

Sequence 118 AA;

Query Match 100.0%; Score 27; DB 21; Length 118;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||||
 Db 31 DYVIN 35

RESULT 8
 AAY51143
 ID AAY51143 standard; Protein; 118 AA.
 XX

AC AAY51143;
 XX
 DT 31-MAR-2000 (first entry)
 XX

DE Murine derived protein fragment #5.
 XX

KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 XX

OS Mus sp.
 XX

PN WO9961629-A1.
 XX

PD 02-DEC-1999.
 XX

PF 24-MAY-1999; 99WO-JP02711.
 XX

PR 25-MAY-1998; 98JP-0159957.
 XX

PR 26-MAY-1998; 98JP-0163023.
 XX

PA (ASAH) ASahi KASEI KOGYO KK.
 PA (ASAH) ASahi MEDICAL CO LTD.
 XX

PI Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI; 2000-086720/07.

DR Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells -
 XX
 XX Disclosure; Page 94-95; 11pp; Japanese.

CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 XX

SQ Sequence 118 AA;

Query Match 100.0%; Score 27; DB 21; Length 118;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||||
 Db 31 DYVIN 35

RESULT 9
 AAY51145

ID AAY51145 standard; Protein; 118 AA.
 XX

AC AAY51145;
 XX

DT 31-MAR-2000 (first entry)
 XX

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DE Murine derived protein fragment #7.
XX Cluster differentiation: cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; murine.
XX MUS sp.
XX WO9961629-A1.
XX 02-DEC-1999.
XX 24-MAY-1999; 99WO-JP02711.
XX 25-MAY-1998; 98JP-0159957.
XX 26-MAY-1998; 98JP-0163023.
XX (ASAH) ASAHI KASEI KOGYO KK.
XX (ASAH) ASAHI MEDICAL CO LTD.
XX Ono M, Soka T, Morimoto I, Miyamura K;
PI WPI; 2000-086720/07.
XX N-PSDB; AA244231.
XX Devices containing antibodies recognising CD4 or CD34 and their use for
XX the separation of CD4 or CD34 positive cells -
XX Disclosure; Page 96-97; 11pp; Japanese.

my pet print

XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for
XX the collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal
XX compositions for the treatment of HIV infection and autoimmune diseases.
XX This sequence represents a murine derived protein fragment which is used
XX to illustrate the method of the invention.

XX Sequence 118 AA;
Query Match 100.0%; Score 27; DB 21; Length 118;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 DYVIN 5
|
31 DYVIN 35

RESULT 10
AAR04135
ID AAR04135 standard; protein; 122 AA.
XX AAR04135;
XX 06-SEP-1990 (first entry)
XX Anti-Leu 3a heavy chain variable region gene product, KOL/316 Vh.
XX HIV; AIDS; anti-Leu3A; vaccine; ds.
XX Mus musculus.
XX EP365209-A.
XX 25-APR-1990.
XX 11-OCT-1989; 89EP-0010415.
XX 17-OCT-1988; 88US-0260558.
XX

XX (BECT) BECTON DICKINSON CO.
XX Hinton R, Oi VT;
XX WPI; 1990-126329/17.
XX N-PSDB; AAQ04042.
XX New chimeric variants of murine antibody anti-leucine -
XX contg. human antibody regions, and DNA encoding sequences.
XX Claim 5; Fig 5; 12pp; English.
XX Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
XX used to form chimeric mouse-variable, human-constant region Abs
XX suggested as being useful as a vaccine to HIV.
XX Sequence 122 AA;
Query Match 100.0%; Score 27; DB 11; Length 122;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 DYVIN 5
|
35 DYVIN 39

RESULT 11
AAB64639
ID AAB64639 standard; Protein; 131 AA.
XX AAB64639;
XX 22-MAR-2001 (first entry)
XX Human secreted protein BLAST search protein SEQ ID NO: 149.
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX anti-allergic; hepatotrophic; antidiabetic; antiinflammatory; antileukic;
XX vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein.
XX Homo sapiens.
XX WO200077197-A1.
XX 21-DEC-2000.
XX 01-JUN-2000; 2000WO-US14934.
XX 11-JUN-1999; 99US-0138599.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
XX Rosen CA, Ruben SM, Komatsoulis GA;
XX WPI; 2001-032312/04.
XX Isolated nucleic acid molecule encoding a human secreted protein is
XX used in preventing, treating or ameliorating a medical condition -
XX Disclosure; Page 534; 558pp; English.

XX The invention relates to the isolation of genes AAF32757-F32803 encoding
XX the human secreted proteins AAB64549-B64594. The sequence is a search
XX result from a BLASTX homology search. The genes and proteins are useful
XX for preventing, ameliorating or treating medical conditions, e.g. by
XX protein or gene therapy. The genes are isolated from a range of human
XX tissues disclosed in the specification. The nucleic acids, proteins,
XX antibodies and (ant)agonists are useful in the diagnosis, treatment

CC and prevention of: (a) cancer, e.g. breast and ovarian cancer, and
 CC other cancers of the adrenal gland, bone, bone marrow, breast,
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 CC and (f) infectious diseases such as viral, bacterial, fungal and
 CC parasitic infections.
 SQ Sequence 131 AA;

Query Match 100.0%; Score 27; DB 22; Length 131;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 Db 66 DYVIN 70

ULT 12
 AAR04133
 ID AAR04133 standard; protein; 136 AA.
 AC AAR04133;
 XX
 DT 06-SEP-1990 (first entry)
 DE Anti-Leu 3a heavy chain variable region gene product, 316 Vh.
 KW HIV; AIDS; anti-Leu3A; vaccine; ds.
 OS Mus musculus.
 XX
 PN EP365209-A.
 XX
 PD 25-APR-1990.
 XX
 PF 11-OCT-1989; 89EP-ON10415.
 PR 17-OCT-1988; 88US-0260558.
 XX
 PA (BECT) BECTON DICKINSON CO.
 XX
 PI Hinton R, Oi VT;
 XX
 DR WPI; 1990-126329/17.
 N-PSDB; AAR04040.

New chimeric variants of murine antibody anti-leucine -
 contg. human antibody regions, and DNA encoding sequences.
 Claim 2; Fig 3; 12pp; English.

Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
 used to form chimeric mouse-variable, human-constant region Abs
 suggested as being useful as a vaccine to HIV.

SQ Sequence 136 AA;

Query Match 100.0%; Score 27; DB 11; Length 136;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 Db 49 DYVIN 53

RESULT 13
 ABB68170

ID ABB68170 standard; Protein; 149 AA.
 XX
 AC ABB68170;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 31302.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 pharmaceutical.
 KW Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL12273.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 XX interactions -
 PS Disclosure; SEQ ID NO 31302; 21pp + Sequence Listing; English.
 CC
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 149 AA;

Query Match 100.0%; Score 27; DB 22; Length 149;
 Best Local Similarity 100.0%; Pred. No. 98;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 Db 114 DYVIN 118

RESULT 14
 ABB54572
 ID ABB54572 standard; Protein; 303 AA.
 XX
 AC ABB54572;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Lactococcus lactis protein rlrA.
 XX
 KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
 OS Lactococcus lactis ILL403.
 XX
 PN FR2807446-A1.

us-09-701-001b-1.rag

Fri Feb 14 15:00:47 2003

CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the H chain sequence of the antibody 4H5.

XX
 SQ Sequence 305 AA;
 Query Match 100.0%; Score 27; DB 21; Length 305;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYVIN 5
 Db 179 DYVIN 183

Search completed: February 14, 2003, 11:15:41
 Job time : 14.5484 secs

XX PD 12-OCT-2001.
 XX PF 11-APR-2000; 2000FR-0004630.
 XX PR 11-APR-2000; 2000FR-0004630.
 XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
 XX Bolotine A, Sorokine A, Renault P, Ehrlich SD;
 XX WPI; 2002-043418/06.
 XX New nucleotide sequence useful in the identification of Lactococcus
 PT lactis and related species -
 XX Claim 6; SEQ ID No 1274; 2504pp; French.

The present invention is related to a Lactococcus lactis nucleotide
 sequence (ABA90521) and related proteins (ABB53300-ABB55621). The
 nucleic acid sequence is useful in the detection and/or amplification of
 nucleic acid sequence, particularly to identify Lactococcus lactis or
 related species. The proteins of the invention are useful for the
 biosynthesis or biodegradation of a composition of interest. The
 invention helps research in lactic bacteria, particularly useful in the
 production of yogurt and cheese.
 CC Note: The sequence data for this patent is based on equivalent patent
 CC WO200177334 (published 18-OCT-2001) which is available in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_ptc_sequences.

XX SQ Sequence 303 AA;
 Query Match 100.0%; Score 27; DB 23; Length 303;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

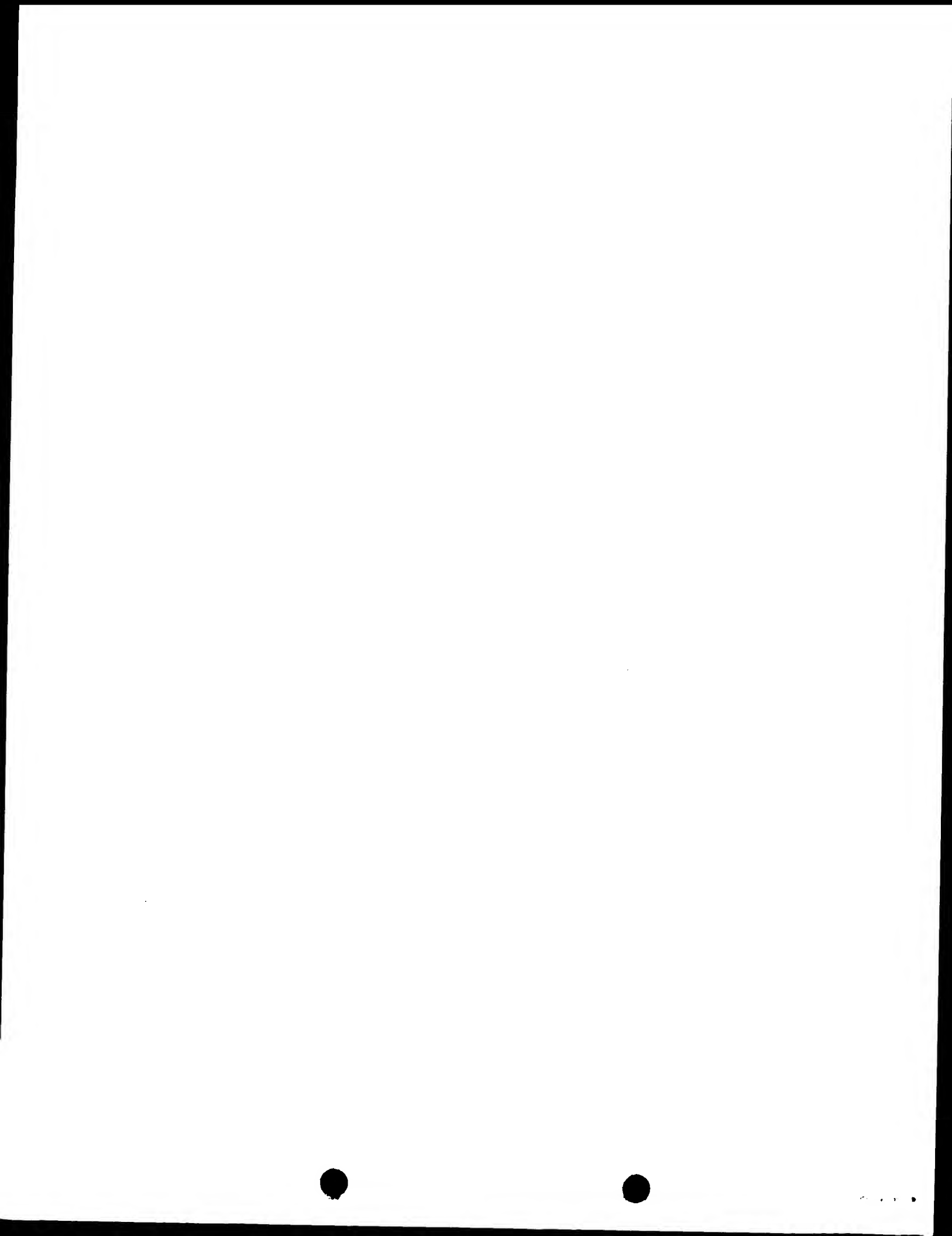
Oy 1 DYVIN 5
 Db 209 DYVIN 213

RESULT 15
 AAY59264
 ID AAY59264 standard; protein; 305 AA.

XX AC AAY59264;
 DE 17-APR-2000 (first entry)
 XX Antibody 4H5 H chain sequence.
 KW CD4 antigen; anti-human; antibody; 4H5; drug.
 OS Mus sp.

XX JPI1332563-A.
 XX 07-DEC-1999.
 XX 26-MAY-1998; 98JP-0163034.
 XX 26-MAY-1998; 98JP-0163034.
 XX (ASAH) ASAH KASEI KOGYO KK.
 XX WPI; 2000-091351/08.
 XX N-PSDB; AAZ58663.

XX An antibody and the nucleic acid coding the antibody -
 PT Disclosure; Page 16-17; 25pp; Japanese.
 XX The invention provides an antibody having affinity to CD4 antigen. The



Fri Feb 14 15:00:48 2003

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:13:07 ; Search time 4.51613 Seconds
(without alignments)
32.575 Million cell updates/sec

Title: US-09-701-001B-1
Perfect score: 27
Sequence: 1 DYVIN 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AA-
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2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	27	100.0	366	2	US-08-804-699-2
2	27	100.0	990	4	US-09-627-376-7
3	26	96.3	215	4	US-09-247-373B-42
4	26	96.3	233	4	US-09-134-001C-3845
5	26	96.3	288	2	US-08-875-062-1
6	26	96.3	338	1	US-08-606-888A-3
7	26	96.3	340	2	US-08-355-844-1
8	26	96.3	340	5	PCT-US95-16126-1
9	26	96.3	462	3	US-09-238-796-2
10	26	96.3	525	4	US-09-113-750A-35
11	26	96.3	575	1	US-08-403-866-7
12	26	96.3	800	2	US-08-785-052-4
13	26	96.3	800	2	US-08-913-581-4
14	26	96.3	990	2	US-08-352-625-20
15	26	96.3	990	2	US-08-466-961A-20
16	26	96.3	990	2	US-08-645-193B-15
17	26	96.3	2404	4	US-09-134-001C-3464
18	25	92.6	7	6	5204096-28
19	25	92.6	127	4	US-09-134-001C-3983
20	25	92.6	234	4	US-09-384-162-9
21	25	92.6	327	4	US-09-134-001C-4937
22	25	92.6	368	1	US-08-423-399B-35
23	25	92.6	387	3	US-08-935-263-6
24	25	92.6	387	4	US-09-594-185-6
25	25	92.6	393	1	US-08-423-399B-33
26	25	92.6	393	1	US-08-530-950-11
27	25	92.6	393	4	US-08-888-429A-11

28	25	92.6	393	4	US-09-149-879-11	Sequence 11, Appl
29	25	92.6	400	1	US-08-530-950-12	Sequence 12, Appl
30	25	92.6	400	2	US-08-878-989-3	Sequence 3, Appl
31	25	92.6	400	2	US-08-878-989-17	Sequence 17, Appl
32	25	92.6	400	4	US-08-888-429A-12	Sequence 12, Appl
33	25	92.6	400	4	US-09-149-879-12	Sequence 12, Appl
34	25	92.6	400	4	US-09-272-796-3	Sequence 3, Appl
35	25	92.6	400	4	US-09-272-796-17	Sequence 17, Appl
36	25	92.6	417	4	US-09-134-001C-5006	Sequence 5006, Ap
37	25	92.6	522	4	US-08-961-083-120	Sequence 120, App
38	25	92.6	736	4	US-09-738-884-2	Sequence 98, Appl
39	25	92.6	749	4	US-09-562-737-98	Sequence 118, App
40	25	92.6	1040	4	US-08-961-083-118	Sequence 32, Appl
41	25	92.6	2544	2	US-08-576-626A-32	Sequence 3182, Ap
42	24	88.9	223	4	US-09-134-001C-3182	Sequence 2, Appl
43	24	88.9	296	3	US-08-986-769-2	Sequence 5053, Ap
44	24	88.9	362	4	US-09-134-001C-5053	Sequence 3952, Ap
45	24	88.9	391	4	US-09-134-001C-3952	

ALIGNMENTS

RESULT 1
US-08-804-699-2
; Sequence 2, Application US/08804699
; Patent No. 5854035
; GENERAL INFORMATION:
; APPLICANT: STOYAN, TANJA
; APPLICANT: KULA, MARIA-REGINA
; TITLE OF INVENTION: ENZYME WITH LEUDH ACTIVITY, NUCLEOTIDE
; TITLE OF INVENTION: SEQUENCE CODING THEREFOR AND PROCESS FOR THE PREPARATION
; NUMBER OF INVENTIONS: OF THE ENZYME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO, L.L.P.
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,699
; FILING DATE: 21-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: JOYCE, KEVIN E
; REGISTRATION NUMBER: 20,508
; REFERENCE/DOCKET NUMBER: 21123/235920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-804-699-2

Query Match 100.0%; Score 27; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYVIN 5
Db 285 DYVIN 289

RESULT 2

US-09-627-376-7
; Sequence 7, Application US/09627376
; Patent No. 6342385
; GENERAL INFORMATION:
; APPLICANT: Qi, Fengxia Caulfield, Page Chen, Ping
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17402/22
; CURRENT APPLICATION NUMBER: US/09/627,376
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 990
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-627-376-7

Query Match 100.0%; Score 27; DB 4; Length 990;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYVIN 5
 |||||
Db 185 DYVIN 189

RESULT 3

US-09-247-373B-42
; Sequence 42, Application US/09247373B
; Patent No. 6168954
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1108-A
; CURRENT APPLICATION NUMBER: US/09/247,373B
; CURRENT FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 08/924,747
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 42
; LENGTH: 215
; TYPE: PRT
; ORGANISM: SOYBEAN
US-09-247-373B-42

Query Match 96.3%; Score 26; DB 4; Length 215;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||||
Db 173 DYVIN 177

RESULT 4

US-09-134-001C-3845
; Sequence 3845, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3845
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3845

Query Match 96.3%; Score 26; DB 4; Length 233;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||||
Db 219 DYVIN 223

RESULT 5

US-08-875-062-1
; Sequence 1, Application US/08875062B
; Patent No. 5942431
; GENERAL INFORMATION:
; APPLICANT: YONEDA, TADASHI
; APPLICANT: HARUM, TAKADA
; APPLICANT: KEI, OHNO
; APPLICANT: JUNJI, SASUGA
; TITLE OF INVENTION: NOVEL LIPASE GENE AND PROCESS FOR THE
; FILE REFERENCE: 5059.204
; CURRENT APPLICATION NUMBER: US/08/875,062B
; CURRENT FILING DATE: 1997-07-10
; EARLIER APPLICATION NUMBER: PCT/JP96/00426
; EARLIER FILING DATE: 1996-02-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
US-08-875-062-1

Query Match 96.3%; Score 26; DB 2; Length 288;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||||
Db 191 DYVIN 195

RESULT 6

US-08-606-888A-3
; Sequence 3, Application US/08606888A
; Patent No. 5766913
; GENERAL INFORMATION:
; APPLICANT: Lin, Shuen-Fuh
; APPLICANT: Chiou, Chien-Ming
; APPLICANT: Chuang, Kuang-Hsiang
; TITLE OF INVENTION: CLONING, EXPRESSION AND NUCLEOTIDE
; TITLE OF INVENTION: SEQUENCE OF A AKALINE GENE FROM PSEUDOMONAS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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;
; ORGANISM: Escherichia coli
;
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..340
; OTHER INFORMATION: OmpF porin protein
;
US-08-355-844-1
Query Match 96.3%; Score 26; DB 2; Length 340;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYVIN 5
Db 312 DYVIN 316

RESULT 8
PCT-US95-16126-1
; Sequence 1, Application PC/TUS9516126
; GENERAL INFORMATION:
; APPLICANT: Fischbarg, Jorge
; APPLICANT: Czegledy, Ferenc
; APPLICANT: Iserovich, Pavel
; APPLICANT: Li, Jun
; APPLICANT: Cheung, Min
; TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16126
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/355,844
; FILING DATE: 14-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Tang, Henry Y.S.
; REGISTRATION NUMBER: 29,705
; REFERENCE/DOCKET NUMBER: A29927-50/29910
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2586
; TELEFAX: 212-765-2519
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..340
; OTHER INFORMATION: OmpF porin protein
;
PCT-US95-16126-1
Query Match 96.3%; Score 26; DB 5; Length 340;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,888A
; FILING DATE: 26-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Rocky Y.
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 06840/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-8906
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
08-606-888A-3
Query Match 96.3%; Score 26; DB 1; Length 338;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYVIN 5
Db 241 DYVIN 245

RESULT 7
US-08-355-844-1
; Sequence 1, Application US/08355844
; Patent No. 5940307
; GENERAL INFORMATION:
; APPLICANT: Fischbarg, Jorge
; APPLICANT: Czegledy, Ferenc
; APPLICANT: Iserovich, Pavel
; APPLICANT: Li, Jun
; APPLICANT: Cheung, Min
; TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/355,844
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Tang, Henry Y.S.
; REGISTRATION NUMBER: 29,705
; REFERENCE/DOCKET NUMBER: A29927-50/29910
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2586
; TELEFAX: 212-765-2519
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:

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QY 1 DYVIN 5
 Db 312 DYIIN 316

RESULT 9
 US-09-238-796-2
 ; Sequence 2, Application US/09238796
 ; Patent No. 6074845
 ; GENERAL INFORMATION:
 ; APPLICANT: AIYAR, NAMBI V.
 ; TITLE OF INVENTION: BECLR:BOVINE CALCITONIN RECEPTOR-LIKE
 ; TITLE OF INVENTION: RECEPTOR
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ratner & Prestia
 ; STREET: P.O. Box 980
 ; CITY: Valley Forge
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19482

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/238,796
 ; FILING DATE: 28-JAN-1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Prestia, Paul F
 ; REGISTRATION NUMBER: 23,031
 ; REFERENCE/DOCKET NUMBER: GP-70599
 ; TELEPHONE: 610-407-0700
 ; TELEFAX: 610-407-0700
 ; TELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 462 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; 09-238-796-2

Query Match 96.3%; Score 26; DB 3; Length 462;
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 Db 367 DYIIN 371

RESULT 10
 US-09-113-750A-35
 ; Sequence 35, Application US/09113750A
 ; Patent No. 6294176
 ; GENERAL INFORMATION:
 ; APPLICANT: David E. Junker and Mark D. Cochran
 ; TITLE OF INVENTION: Recombinant Raccoonpox virus
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: John P. White
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York

; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/113,750A
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 55744
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)262-0400
 ; TELEFAX: (212)664-0525
 ; TELEX: 422523
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 525 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-09-113-750A-35

Query Match 96.3%; Score 26; DB 4; Length 525;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 Db 485 DYIIN 489

RESULT 11
 US-08-403-866-7
 ; Sequence 7, Application US/08403866
 ; Patent No. 5643779
 ; GENERAL INFORMATION:
 ; APPLICANT: Ehrlich, Stanislaw
 ; APPLICANT: Godon, Jean-Jacques
 ; APPLICANT: Renault, Pierre
 ; TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
 ; TITLE OF INVENTION: synthase from Lactococcus and its applications
 ; NUMBER OF SEQUENCES: 16
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/403,866
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Goldman, Michael L.
 ; REGISTRATION NUMBER: 30,727
 ; REFERENCE/DOCKET NUMBER: 20747/30
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (716) 263-1600
 ; TELEFAX: (716) 263-1487
 ; TELEX: 978450 (WUT)
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 575 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:

us-09-701-001b-1.ra1

Fri Feb 14 15:00:48 2003

ORGANISM: Lactococcus lactis subsp. lactis
INDIVIDUAL ISOLATE: ILVB
US-08-403-866-7

Query Match 96.3%; Score 26; DB 1; Length 575;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 278 DYIN 282

RESULT 12

US-08-785-052-4
Sequence 4, Application US/08785052
Patent No. 5756329

GENERAL INFORMATION:
APPLICANT: Hodgson, John
TITLE OF INVENTION: NO. 5756329el tRNA synthetase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,052
FILING DATE: 17-JAN-1997

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9601096.2
FILING DATE: 19-JAN-1996

APPLICATION NUMBER: 9615845.6
FILING DATE: 27-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimml, Edward R

REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31354-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090

TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 800 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-785-052-4

Query Match 96.3%; Score 26; DB 1; Length 800;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 607 DYVN 611

RESULT 13

US-08-913-581-4
Sequence 4, Application US/08913581
Patent No. 5948657

GENERAL INFORMATION:
APPLICANT: Entian, Karl-Dieter
APPLICANT: G tz, Friedrich
APPLICANT: Schnell, No. 5837485bert
APPLICANT: Augustin, Johannes
APPLICANT: Engelke, Germar
APPLICANT: Rosenstein, Ralf
APPLICANT: Kaletta, Cortina
APPLICANT: Klein, Cora
APPLICANT: Wieland, Bernd
APPLICANT: Kupke, Thomas
APPLICANT: Jung, G nther
APPLICANT: Kellner, Roland
TITLE OF INVENTION: Biosynthetic Process For The Preparation
OF Chemical Compounds

Query Match 96.3%; Score 26; DB 1; Length 800;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 607 DYVN 611

RESULT 14

US-08-392-625-20
Sequence 20, Application US/08392625
Patent No. 5837485

GENERAL INFORMATION:
APPLICANT: Entian, Karl-Dieter
APPLICANT: G tz, Friedrich
APPLICANT: Schnell, No. 5837485bert
APPLICANT: Augustin, Johannes
APPLICANT: Engelke, Germar
APPLICANT: Rosenstein, Ralf
APPLICANT: Kaletta, Cortina
APPLICANT: Klein, Cora
APPLICANT: Wieland, Bernd
APPLICANT: Kupke, Thomas
APPLICANT: Jung, G nther
APPLICANT: Kellner, Roland
TITLE OF INVENTION: Biosynthetic Process For The Preparation
OF Chemical Compounds

Query Match 96.3%; Score 26; DB 2; Length 800;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 607 DYVN 611

; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 ; STREET: 1100 New York Avenue
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/392.625
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/876,791
 ; FILING DATE: 30-APR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Esmond, Robert W.
 ; REGISTRATION NUMBER: 32,893
 ; REFERENCE/DOCKET NUMBER: 0652.0980002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 990 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-392-625-20

Query Match 96.3%; Score 26; DB 2; Length 990;
 Best Local Similarity 80.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 DB 248 DYIIN 252

RESULT 15
 US-08-466-961A-20
 ; Sequence 20, Application US/08466961A
 ; Patent No. 5843709
 ; GENERAL INFORMATION:
 ; APPLICANT: Entian, Karl-Dieter
 ; APPLICANT: G tz, Friedrich
 ; APPLICANT: Schnell, No. 5843709bert
 ; APPLICANT: Augustin, Johannes
 ; APPLICANT: Engelke, Gernar
 ; APPLICANT: Rosenstein, Ralf
 ; APPLICANT: Kaletta, Cortina
 ; APPLICANT: Klein, Cora
 ; APPLICANT: Wieland, Bernd
 ; APPLICANT: Kupke, Thomas
 ; APPLICANT: Jung, G nther
 ; APPLICANT: Kellner, Roland
 ; TITLE OF INVENTION: Biosynthetic Process for the Preparation of
 ; TITLE OF INVENTION: Chemical Compounds
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 ; STREET: 1100 New York Avenue, NW
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/466,961A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/392.625
 ; FILING DATE: 22-FEB-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/876,791
 ; FILING DATE: 30-APR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/784,234
 ; FILING DATE: 31-OCT-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Esmond, Robert W.
 ; REGISTRATION NUMBER: 32,893
 ; REFERENCE/DOCKET NUMBER: 0652.0980004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 990 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-466-961A-20

Query Match 96.3%; Score 26; DB 2; Length 990;
 Best Local Similarity 80.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 DB 248 DYIIN 252

Search completed: February 14, 2003, 11:20:47
 Job time : 5.51613 secs

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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:15:53 : Search time 2.90323 Seconds
(without alignments)
44.001 Million cell updates/sec

Title: US-09-701-001b-1

Perfect score: 27

Sequence: 1 DYVIN 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap.*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	399	10	US-09-925-301-1385
2	27	100.0	990	12	US-10-047-676A-7
3	26	96.3	139	10	US-09-815-242-10702
4	26	96.3	343	10	US-09-815-242-5705
5	26	96.3	354	10	US-09-815-242-12464
6	26	96.3	658	10	US-09-815-242-10947
7	26	96.3	792	10	US-09-815-242-5411
8	26	96.3	800	10	US-09-815-242-12366
9	26	96.3	801	10	US-09-815-242-12985
10	26	96.3	801	10	US-09-815-242-4879
11	26	96.3	1167	10	US-09-815-242-11522
12	26	96.3	1349	10	US-09-815-242-5898
13	26	96.3	1349	10	US-09-815-242-13137
14	25	92.6	118	10	US-09-905-243-70
15	25	92.6	228	10	US-09-755-665-38
16	25	92.6	276	10	US-09-815-242-13118
17	25	92.6	306	10	US-09-815-242-5895
18	25	92.6	364	10	US-09-755-665-64
19	25	92.6	387	12	US-10-033-078-6

Sequence 36, Appl
Sequence 11, Appl
Sequence 34, Appl
Sequence 12, Appl
Sequence 5329, Ap
Sequence 12188, A
Sequence 12845, A
Sequence 381, App
Sequence 120, App
Sequence 69, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 118, App
Sequence 5620, App
Sequence 12543, A
Sequence 31, Appl
Sequence 5047, Ap
Sequence 11770, A
Sequence 10149, A
Sequence 13845, A
Sequence 88, Appl
Sequence 13561, A
Sequence 126, App
Sequence 2, Appl
Sequence 4, Appl
Sequence 3, Appl

20 92.6 10 US-09-755-665-36
21 92.6 10 US-09-761-569-11
22 92.6 10 US-09-755-665-34
23 92.6 10 US-09-761-569-12
24 92.6 10 US-09-815-242-5329
25 92.6 10 US-09-815-242-12188
26 92.6 10 US-09-815-242-12845
27 92.6 10 US-09-912-020-381
28 92.6 10 US-09-765-273-120
29 92.6 10 US-09-888-615-69
30 92.6 9 US-10-096-961-2
31 92.6 10 US-09-800-971-2
32 92.6 10 US-09-765-272-118
33 92.6 10 US-09-815-242-5620
34 88.9 10 US-09-815-242-12543
35 88.9 10 US-09-775-925-31
36 88.9 10 US-09-815-242-5047
37 88.9 10 US-09-815-242-11770
38 88.9 10 US-09-815-242-10149
39 88.9 10 US-09-815-242-13845
40 88.9 9 US-10-260-877-88
41 88.9 10 US-09-815-242-13561
42 88.9 9 US-09-989-442-126
43 88.9 9 US-10-098-514-2
44 88.9 9 US-10-098-514-4
45 88.9 9 US-09-978-756-3

ALIGNMENTS

RESULT 1
US-09-925-301-1385
; Sequence 1385, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL06
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1385
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1385

Query Match 100.0%; Score 27; DB 10; Length 399;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 304 DYVIN 308
|||||

RESULT 2
US-10-047-676A-7
; Sequence 7, Application US/10047676A
; Patent No. US20020123105A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Fengxia
; APPLICANT: Caulfield, Page W.
; APPLICANT: Chen, Ping W.
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17403/22
; CURRENT APPLICATION NUMBER: US/10/047,676A

; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 09/627,376
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 990
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-047-676A-7

Query Match 100.0%; Score 27; DB 12; Length 990;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 185 DYVIN 189

RESULT 3
US-09-815-242-10702
Sequence 10702, Application US/09815242
; Patent No. US20020061569A1

; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes

; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10702
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10702

Query Match 96.3%; Score 26; DB 10; Length 139;
Best Local Similarity 80.0%; Pred. No. 40;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 17 DYVIN 21

RESULT 4
US-09-815-242-5705
Sequence 5705, Application US/09815242
; Patent No. US20020061569A1

; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; TITLE OF INVENTION: Prokaryotes

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5705

; LENGTH: 343

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-09-815-242-5705

Query Match 96.3%; Score 26; DB 10; Length 343;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 210 DYVIN 214

RESULT 5

US-09-815-242-12464

; Sequence 12464, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; TITLE OF INVENTION: Prokaryotes

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

us-09-701-001b-1.rapb

Fri Feb 14 15:00:48 2003

PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 12464
 LENGTH: 354
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-09-815-242-12464

Query Match 96.3%; Score 26; DB 10; Length 354;
 Best Local Similarity 80.0%; Pred. No. 1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||:|
 213 DYVIN 217

RESULT 6
 US-09-815-242-10947
 ; Sequence 10947, Application US/09815242
 ; Patent No. US20020061569A1

GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 TITLE OF INVENTION: Identification of Essential Genes in
 TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 10947
 LENGTH: 658
 TYPE: PRT
 ORGANISM: Enterococcus faecalis
 US-09-815-242-10947

Query Match 96.3%; Score 26; DB 10; Length 658;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||:|
 76 DYVIN 80

RESULT 7
 US-09-815-242-5411
 ; Sequence 5411, Application US/09815242

Patent No. US20020061569A1
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 5411
 LENGTH: 792
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-09-815-242-5411

Query Match 96.3%; Score 26; DB 10; Length 792;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||:|
 607 DYVIN 611

RESULT 8
 US-09-815-242-12366
 ; Sequence 12366, Application US/09815242
 ; Patent No. US20020061569A1

GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625

```

; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12366
; LENGTH: 800
; TYPE: prt
; ORGANISM: Staphylococcus aureus
US-09-815-242-12366

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Query Match 95.3%; Score 26; DB 10; Length 800;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels

ULT 9
 US-09-815-242-12985
 ; Sequence 12985, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haseibeck, Robert
 ; APPLICANT: Ohlsen, Karl L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard

Query Match 96.38; Score 26; DB 10; Length 800;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels

RESULT 10
US-09-815-242-4879

```

; Sequence 4879, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
;

```

Query Match 96.3%; Score 26; DB 10; Length 801;
Best Local Similarity 80.0%; Pred. NO. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels

```

RESULT 11
US-09-815-242-11522
; Sequence 11522, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.

```

```

, , CURRENT APPLICATION NUMBER: US/09/915,242
, , CURRENT FILING DATE: 2001-03-21
, , PRIOR APPLICATION NUMBER: 60/191,078
, , PRIOR FILING DATE: 2000-03-21
, , PRIOR APPLICATION NUMBER: 60/206,848
, , PRIOR FILING DATE: 2000-05-23
, , PRIOR APPLICATION NUMBER: 60/207,727
, , PRIOR FILING DATE: 2000-05-26
, , PRIOR APPLICATION NUMBER: 60/242,578
, , PRIOR FILING DATE: 2000-10-23

```

RESULT 10
US-09-815-242-4879

Fri Feb 14 15:00:48 2003

```

; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11522
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11522

Query Match          96.3%; Score 26; DB 10; Length 1167;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 DYVIN 5
11111
Db 1101 DYVIN 1105

RESULT 12
US-09-815-242-5898
; Sequence 5898, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13137
; LENGTH: 1349
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13137

Query Match          96.3%; Score 26; DB 10; Length 1349;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5
11111
Db 395 DYVIN 399

RESULT 14
US-09-905-243-70
; Sequence 70, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rat/chimpanzee sequence
US-09-905-243-70

Query Match          92.6%; Score 25; DB 10; Length 118;
Best Local Similarity 80.0%; Pred. No. 56;

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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
||:|
Db 31 DYVLN 35

RESULT 15
US-09-755-665-38
; Sequence 38, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Spyttek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 38
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-38

Query Match 92.6%; Score 25; DB 10; Length 228;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
||:|
Db 154 DYVIN 158

Search completed: February 14, 2003, 11:21:29
Job time : 3.90323 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:12:02 ; Search time 5 Seconds
(without alignments)

96.134 Million cell updates/sec

Title: US-09-701-001B-1

Perfect score: 27

Sequence: 1 DYVIN 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	162	1 CFMWA	C-phycocyanin alph
2	27	100.0	162	2 T06968	C-phycocyanin alph
3	27	100.0	164	2 G45045	phycoerythrin I al
4	27	100.0	164	2 B35127	phycoerythrin alph
5	27	100.0	164	2 B47207	phycoerythrin I al
6	27	100.0	164	2 S43779	phycoerythrin clas
7	27	100.0	165	2 A40007	phycoerythrin alph
8	27	100.0	165	2 S25318	adenylate kinase (
9	27	100.0	217	2 J50492	adenylate kinase (
10	27	100.0	217	2 T44404	purine nucleoside
11	27	100.0	231	2 D69980	hypothetical prote
12	27	100.0	259	2 G81833	hypothetical prote
13	27	100.0	299	2 C90519	LysR family transc
14	27	100.0	303	2 D86779	leucine dehydrogen
15	27	100.0	341	2 F83217	hypothetical prote
16	27	100.0	345	2 E84051	alcohol dehydrogen
17	27	100.0	347	1 A44245	alcohol dehydrogen
18	27	100.0	347	1 S51120	probable dehydroge
19	27	100.0	348	1 H71110	L-threonine 3-dehy
20	27	100.0	348	2 G75049	Glu/Leu/Phe/Val de
21	27	100.0	353	2 A87507	leucine dehydrogen
22	27	100.0	353	2 A11859	probable leucine d
23	27	100.0	364	1 B69962	leucine dehydrogen
24	27	100.0	364	2 E83995	leucine dehydrogen
25	27	100.0	366	2 S45607	spermine synthase
26	27	100.0	368	2 S54160	hypothetical prote
27	27	100.0	376	2 A89957	hypothetical prote
28	27	100.0	378	2 T25885	probable type I re
29	27	100.0	380	2 E81302	

30	27	100.0	386	2 D83284	probable acyl-CoA
31	27	100.0	403	2 E70618	probable fadE2 pro
32	27	100.0	418	2 A97300	gamma-glutamyl pho
33	27	100.0	423	2 T15350	hypothetical prote
34	27	100.0	429	1 A31950	leucine dehydrogen
35	27	100.0	431	2 T36129	probable PIS trans
36	27	100.0	488	2 H71452	hypothetical prote
37	27	100.0	492	2 A97429	flgK protein prote
38	27	100.0	492	2 AB2647	hook associated pr
39	27	100.0	499	2 T32337	hypothetical prote
40	27	100.0	584	2 S27500	xylanase - Prevote
41	27	100.0	587	2 T27765	hypothetical prote
42	27	100.0	610	2 T35222	hypothetical prote
43	27	100.0	638	1 KQMSPL	plasma kallikrein
44	27	100.0	703	2 AC2430	hypothetical prote
45	27	100.0	705	2 S76729	hypothetical prote

ALIGNMENTS

RESULT 1

CFMWA

C-phycocyanin alpha chain - Fischerella sp.

C:Species: Fischerella sp.

C:Date: 30-Jun-1979 #sequence_revision 30-Jun-1979 #text_change 30-Apr-1999

C:Accession: A00315

R:Frank, G.; Sidler, W.; Widmer, H.; Zuber, H.

Hoppe-Sevler's Z. Physiol. Chem. 359, 1491-1507, 1978

A:Title: The complete amino acid sequence of both subunits of C-phycocyanin from the

A:Reference number: A00315; MUID:79087164; PMID:103794

A:Accession: A00315

A:Molecule type: protein

A:Residues: 1-162 <FRA>

A:Note: the source was designated as Mastigocladus laminosus

C:Superfamily: phycocyanin

C:Keywords: chromoprotein; photosynthesis; phycocyanobilin

F;84/Binding site: phycocyanobilin (Cys) (covalent) #status experimental

Query Match 100.0%; Score 27; DB 1; Length 162;

Best Local Similarity 100.0%; Pred. No. 76;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5

Db 155 DYVIN 159

RESULT 2

T06968

C-phycocyanin alpha chain - Cyanophora paradoxa cyanelle

C:Species: cyanelle Cyanophora paradoxa

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jun-1999

C:Accession: T06968; A24650

R:Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohmert, H.J.; Bryant, D.A.

submitted to the EMBL Data Library, July 1995

A:Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.

A:Reference number: Z15840

A:Accession: T06968

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-162 <STI>

A:Cross-references: EMBL:U30821; NID:g1016083; PIDN:AAA81311.1; PID:g1016224

A:Experimental source: strain Pringsheim LB555

R:Lemaux, P.G.; Grossman, A.R.

EMBO J. 4, 1911-1919, 1985

A:Title: Major light-harvesting polypeptides encoded in polycistronic transcripts in

A:Reference number: A91009; MUID:86055745; PMID:2998775

A:Accession: A24650

A:Molecule type: DNA

A:Residues: 1-15 <LEM>

A:Cross-references: GB:X02790; NID:g11395; PIDN:CAA26557.1; PID:g11386

C:Genetics:

A:Gene: cpca

A:Genome: cyanelle

C:Superfamily: phycocyanin

C:Keywords: chromoprotein; cyanelle; heterodimer; photosynthesis; phycocyanobilin

F:84/Binding site: phycocyanobilin (Cys) (covalent) #status predicted

Query Match

Best Local Similarity 100.0%; Score 27; DB 2; Length 162;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5

|||||

Db 157 DYVIN 159

RESULT 3

G45045 phycoerythrin I alpha chain - *Synechococcus* sp. (strain WH8020)

C:Species: *Synechococcus* sp.

C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jun-1999

C:Accession: G45045; S31055

R:Bernard, C.; Thomas, J.C.; Mazel, D.; Mousseau, A.; Castets, A.M.; Tandeau de Marsa

R:Bernard, C.; Thomas, J.C.; Mazel, D.; Mousseau, A.; Castets, A.M.; Tandeau de Marsa

A:Title: Rod structure of a phycoerythrin II-containing phycobilisome. I. Organization a

A:Reference number: A45045; MUID:93123238; PMID:8419325

A:Accession: G45045

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-164 <WIL>

A:Cross-references: EMBL:M95288; NID:gl154551; PIDN:AAA27340.1; PID:gl154560

A:Experimental source: WH8020

A>Note: sequence extracted from NCBI backbone (NCBIP:121981)

C:Genetics:

A:Gene: cpca

C:Superfamily: phycocyanin

Query Match

Best Local Similarity 100.0%; Score 27; DB 2; Length 164;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5

|||||

Db 157 DYVIN 161

RESULT 4

B35127 phycoerythrin alpha chain - *Synechocystis* sp. (strain PCC 6701)

C:Species: *Synechocystis* sp.

C:Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 11-Jun-1999

C:Accession: B35127

R:Anderson, L.K.; Grossman, A.R.

J. Bacteriol. 172, 1297-1305, 1990

A:Title: Structure and light-regulated expression of phycoerythrin genes in wild-type an

A:Reference number: A35127; MUID:90170840; PMID:2106507

A:Accession: B35127

A:Molecule type: DNA

A:Residues: 1-164 <AND>

A:Cross-references: GB:M33812; NID:gl154457; PIDN:AAA27280.1; PID:gl154459

C:Superfamily: phycocyanin

Query Match

Best Local Similarity 100.0%; Score 27; DB 2; Length 164;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5

|||||

Db 157 DYVIN 161

RESULT 5

B47207

phycoerythrin alpha subunit - red alga (*Rhodella violacea*)

C:Species: *Rhodella violacea*

C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997

C:Accession: B47207

R:Bernard, C.; Thomas, J.C.; Mazel, D.; Mousseau, A.; Castets, A.M.; Tandeau de Marsa

R:Bernard, C.; Thomas, J.C.; Mazel, D.; Mousseau, A.; Castets, A.M.; Tandeau de Marsa

A:Title: Characterization of the genes encoding phycoerythrin in the red alga *Rhodell*

A:Reference number: A47207; MUID:93028502; PMID:1409666

A:Accession: B47207

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-164 <BER>

A>Note: sequence extracted from NCBI backbone (NCBIN:115792, NCBIP:115794)

C:Superfamily: phycocyanin

C:Keywords: chloroplast

Query Match

Best Local Similarity 100.0%; Score 27; DB 2; Length 164;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5

|||||

Db 157 DYVIN 161

RESULT 6

S43779

phycoerythrin I alpha chain - *Synechococcus* sp.

C:Species: *Synechococcus* sp.

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999

C:Accession: S43779; S32642

R:Newman, J.; Mann, N.H.; Carr, N.G.

Plant Mol. Biol. 24, 679-683, 1994

A:Title: Organization and transcription of the class I phycoerythrin genes of the mar

A:Reference number: S43777; MUID:94207193; PMID:7512390

A:Accession: S43779

A:Molecule type: DNA

A:Residues: 1-164 <NEW>

A:Cross-references: EMBL:X72961; NID:g288983; PIDN:CAA51465.1; PID:g288986

C:Genetics:

A:Gene: cpca

C:Superfamily: phycocyanin

Query Match

Best Local Similarity 100.0%; Score 27; DB 2; Length 164;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5

|||||

Db 157 DYVIN 161

RESULT 7

A40007

phycoerythrin class II alpha chain mpeA - *Synechococcus* sp. (strain WH8020)

C:Species: *Synechococcus* sp.

C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 11-Jun-1999

C:Accession: A40007; S31048

R:Wilbanks, S.M.; de Lorimier, R.; Glazer, A.N.

J. Biol. Chem. 266, 9535-9539, 1991

A:Title: Phycoerythrins of marine unicellular cyanobacteria. Sequence of a class II p

A:Reference number: A40007; MUID:91236722; PMID:1903390

A:Accession: A40007

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-165 <WIL>

A:Cross-references: GB:M61118; NID:gl154529; PIDN:AAA27320.1; PID:gl154531; EMBL:M95288

C:Genetics:

A:Gene: mpeA

C:Superfamily: phycocyanin

Query Match

Best Local Similarity 100.0%; Score 27; DB 2; Length 165;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5

|||||

Db 158 DYVIN 162

RESULT 8

S25318

phycoerythrin alpha chain - *Synechococcus* sp.

C:Species: *Synechococcus* sp.

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999

C:Accession: S25318

R:de Lorimier, R.; Chen, C.C.J.; Glazer, A.N.

Plant Mol. Biol. 20, 353-356, 1992

A:Title: Sequence comparison of two highly homologous phycoerythrins differing in bilin

A:Reference number: S25318; MUID:93004492; PMID:1391782

C:Accession: S25318

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-165 <LOR>

A:Cross-references: GB:M91809; NID:gl54532; PIDN:AAA27322.1; PID:gl54534

C:Superfamily: phycocyanin

Query Match 100.0%; Score 27; DB 2; Length 165;

Best Local Similarity 100.0%; Pred. No. 77;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5

|||||

Db 158 DYVIN 162

RESULT 9

JS0492

adenylate kinase (EC 2.7.4.3) - *Bacillus subtilis*

N:Alternate names: ATP-AMP transphosphorylase

C:Species: *Bacillus subtilis*

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C:Accession: JS0492; S12684; S08630; E69583

R:Nakamura, K.; Nakamura, A.; Takamatsu, H.; Yoshikawa, H.; Yanane, K.

J. Biochem. 107, 603-607, 1990

A:Title: Cloning and characterization of a *Bacillus subtilis* gene homologous to E. coli

A:Reference number: JS0490; MUID:90292990; PMID:2113521

A:Accession: JS0492

A:Molecule type: DNA

A:Residues: 1-217 <NAK>

A:Cross-references: GB:D00619; NID:g216336; PIDN:BAA00496.1; PID:g216340

R:Yoshikawa, H.; Doi, R.H.

Nucleic Acids Res. 18, 1647, 1990

A:Title: Sequence of the *Bacillus subtilis* spectinomycin resistance gene region.

A:Reference number: S12680; MUID:90221911; PMID:2139212

A:Accession: S12684

A:Molecule type: DNA

A:Residues: 1-116 <YOS>

A:Cross-references: EMBL:M31102; NID:gl184272; PIDN:AAB59119.1; PID:gl43579

A:Experimental source: strain 1A241

R:Shih, J.W.; Boylan, S.A.; Thomas, S.M.; Dolan, K.M.; Oliver, D.B.; Price, C.W.

Mol. Microbiol. 4, 305-314, 1990

A:Title: Isolation of a *secY* homologue from *Bacillus subtilis*: evidence for a common pro

A:Reference number: S08628; MUID:90251170; PMID:2110998

A:Accession: S08630

A:Molecule type: DNA

A:Residues: 1-99 <SUH>

A:Cross-references: EMBL:X51329; NID:g40132; PIDN:CAA35713.1; PID:g40135

A:Experimental source: strain Marburg; cell line P2

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C:Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A:Erlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

lech, J.; Harwood, C.R.; Henauc, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchida
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtili*
A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: E69583

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-217 <KUN>

A:Cross-references: GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11913.1; PID:g26324

A:Experimental source: strain 168

C:Genetics:

A:Gene: adk

C:Function:

A:Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP

A:Note: magnesium required

C:Superfamily: adenylate kinase

C:Keywords: ATP; P-loop; phosphotransferase

F;7-14/Region: nucleotide-binding motif A (P-loop) #status atypical

F;80-85/Region: nucleotide-binding motif B #status atypical

F;28,84/Active site: His, Asp #status predicted

Query Match 100.0%; Score 27; DB 2; Length 217;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5

|||||

Db 108 DYVIN 112

RESULT 10

T44404

adenylate kinase (EC 2.7.4.3) [imported] - *Bacillus halodurans*

C:Species: *Bacillus halodurans*

C>Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 15-Jun-2001

C:Accession: T44404; C83669

R:Takami, H.; Takaki, Y.; Nakasone, K.; Hirama, C.; Inoue, A.; Horikoshi, K.

Biosci. Biotechnol. Biochem. 63, 452-455, 1999

A:Title: Sequence analysis of a 32-kb region including the major ribosomal protein ge

A:Reference number: Z22756; MUID:99209008; PMID:10192928

A:Accession: T44404

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-217 <TAK>

A:Cross-references: EMBL:AB017508; NID:g4512395; PIDN:BAA75292.1; PID:g4512425

A:Experimental source: strain C-125

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H.

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* a

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: C83669

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-217 <STO>

A:Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BA03874.1; GSPDB:G

A:Experimental source: strain C-125

C:Genetics:

A:Gene: adk

C:Superfamily: adenylate kinase

C:Keywords: phosphotransferase

Query Match 100.0%; Score 27; DB 2; Length 217;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5

|||||

Db 108 DYVIN 112

RESULT 11
 D69980
 purine nucleoside phosphorylase homolog yrrU - Bacillus subtilis
 C:Species: Bacillus subtilis
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
 C:Accession: D69980
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
 Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: D69980
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-231 <KUN>
 A:Cross-references: GB:Z99117; GB:AL009126; NID:g2634966; PIDN:CAB14669.1; PID:g2635173
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yrrU
 C:Superfamily: Escherichia coli pfs protein
 Query Match 100.0%; Score 27; DB 2; Length 231;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DYVIN 5
 Db 69 DYVIN 73
 RESULT 12
 G81833
 hypothetical protein NMA2036 [imported] - Neisseria meningitidis (strain Z2491 serogroup
 C:Species: Neisseria meningitidis
 C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: G81833
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 B.; Lloyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919
 A:Accession: G81833
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-259 <PAR>
 A:Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85255.1; PID:g738066
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: NMA2036
 Query Match 100.0%; Score 27; DB 2; Length 259;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DYVIN 5
 Db 78 DYVIN 82
 RESULT 13

C90519
 hypothetical protein MYP0_0590 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
 C:Species: Mycoplasma pulmonis
 C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
 C:Accession: C90519
 R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer,
 Nucleic Acids Res. 29, 2145-2153, 2001
 A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma p
 A:Reference number: A99512; MUID:21267165; PMID:11353084
 A:Accession: C90519
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-299 <KUR>
 A:Cross-references: GB:AL445566; PID:g14089472; PIDN:CAC13232.1; GSPDB:GN00153
 A:Experimental source: strain UAB CTIP
 C:Genetics:
 A:Gene: MYP0_0590
 A:Genetic code: SGC3
 Query Match 100.0%; Score 27; DB 2; Length 299;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DYVIN 5
 Db 73 DYVIN 77
 RESULT 14
 D86779
 LysR family transcription regulator [imported] - Lactococcus lactis subsp. lactis (st
 C:Species: Lactococcus lactis subsp. lactis
 C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: D86779
 R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Eh
 Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: D86779
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-303 <STO>
 A:Cross-references: GB:AE005176; PID:g12724207; PIDN:AAK05334.1; GSPDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: rlrA
 Query Match 100.0%; Score 27; DB 2; Length 303;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DYVIN 5
 Db 209 DYVIN 213
 RESULT 15
 F83217
 leucine dehydrogenase PA3418 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: F83217
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: F83217
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-341 <STO>
 A:Cross-references: GB:AE004763; GB:AE00491; NID:g9949556; PIDN:AAG06806.1; GSPDB:GN

A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: ldh; PA3418
 C:Superfamily: leucine dehydrogenase

Query Match 100.0%; Score 27; DB 2; Length 341;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||||
 Db 277 DYVIN 281

Search completed: February 14, 2003, 11:19:44
 Job time : 6 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:05:27 ; Search time 2.58065 Seconds
(without alignments)
80.360 Million cell updates/sec

Title: US-09-701-001B-1

Perfect score: 27
Sequence: 1 DYVIN 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Checked: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	162	1 PHCA_CVAPA	P05730 cyanophora
2	27	100.0	162	1 PHCA_MASLA	P00307 mastigoclad
3	27	100.0	164	1 PHAL_SYNPN	Q08086 synechococc
4	27	100.0	164	1 PHAL_SYNPN	Q02179 synechococc
5	27	100.0	164	1 PHEA_GRIMO	Q36005 griffithsia
6	27	100.0	164	1 PHEA_RHOVL	Q02036 rhodella vi
7	27	100.0	164	1 PHEA_SYNY1	P20778 synechocyst
8	27	100.0	165	1 PHA2_SYNPN	P27646 synechococc
9	27	100.0	165	1 PHA2_SYNPN	P37720 synechococc
10	27	100.0	217	1 KAD_BACSU	P38372 bacillus su
11	27	100.0	217	1 KAD_BACSU	P16304 bacillus su
12	27	100.0	231	1 MTN_BACSU	Q32028 bacillus su
13	27	100.0	280	1 ANFD_HEUGE	O68955 heliobacter
14	27	100.0	347	1 ADH_SULSR	P39462 sulfolobus
15	27	100.0	347	1 ADH_SULSR	P50381 sulfolobus
16	27	100.0	364	1 DHLE_BACLI	Q35560 bacillus li
17	27	100.0	364	1 DHLE_BACSU	P54531 bacillus su
18	27	100.0	366	1 DHLE_BACCE	Q59194 bacillus ce
19	27	100.0	366	1 DHLE_THEIN	O60030 thermoactin
20	27	100.0	366	1 SPSY_HUMAN	P32788 homo sapien
21	27	100.0	366	1 SPSY_MOUSE	P97355 mus musculu
22	27	100.0	377	1 DHLE_BACST	P31514 bacillus st
23	27	100.0	418	1 PROA_CLOAB	Q97e62 clostridium
24	27	100.0	423	1 YWV2_CAEEL	Q11076 caenorhabdi
25	27	100.0	587	1 Y548_CAEEL	Q09374 caenorhabdi
26	27	100.0	638	1 KAL_MOUSE	P26262 mus musculu
27	27	100.0	820	1 SYL_CHLPN	Q92930 chlamydia p
28	27	100.0	857	1 GELA_DICDI	P33466 dictyosteli
29	27	100.0	1082	1 RRO_PORPC	P26190 porcine rot
30	26	96.3	162	1 PHA3_FREDI	P14876 fremyella d
31	26	96.3	164	1 PHEA_PORPU	P51368 porphyra pu
32	26	96.3	168	1 RBS_CHLMO	P17537 chlamydomon
33	26	96.3	213	1 CAD1_DICDI	P54657 dictyosteli

RESULT 1
PHCA_CVAPA STANDARD; PRT; 162 AA.
AC P05730;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-phycocyanin alpha chain.
GN CPCA OR PCVA.
OS Cyanophora paradoxa.
OG Cyanelle.
OC Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
OX NCBI_TaxID=2762;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LB555 / Pringsheim;
RA Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
RA Bryant D.A.;
RT "Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";
RL Plant Mol. Biol. Rep. 13:327-332(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LB555 / Pringsheim;
RA Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M.,
RA Farley J.F., Schlachter W.M., Chung S., Newmann-Spallart C.,
RA Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
RT "The complete sequence of the cyanelle genome of Cyanophora paradoxa:
RT the genetic complexity of a primitive plastid.";
RL (In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
RL Schwemmler W. (eds.);
RL Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg
RL (1997).
RN [3]
RP SEQUENCE OF 1-15 FROM N.A.
RC MEDLINE=86055745; PubMed=2998775;
RA Lemaux P.G., Grossman A.R.;
RT "Major light-harvesting polypeptides encoded in polycistronic
transcripts in a eukaryotic alga.";
RL EMOB J. 4:1911-1919(1985).
CC -1- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
CC FROM THE PHYCOBILIPROTEIN COMPLEX.
CC -1- SURUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
CC -----
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CC -----
CC EMBL; U30821; AAA81311.1;
CC PIR; A24650; A24650.
CC HSP; P00306; 1PHN.

P17576 polyporus t
O53872 streptomyce
P02931 escherichia
O69056 streptomyce
Q06539 streptomyce
P40176 streptomyce
Q9uzw0 pyrococcus
O58965 pyrococcus
P42609 escherichia
P14898 dictyoglomu
Q02137 lactococcus
P38882 saccharomyc

ALIGNMENTS

```

QY      1 DYVIN 5
DB      155 DYVIN 159

RESULT 3
PHAL_SYNPW
ID PHAL_SYNPW STANDARD; PRT; 164 AA.
AC Q08086;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-phycoerythrin class I alpha chain.
GN CPEA.
OS Synechococcus sp. (strain WH7803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32051;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94207193; PubMed=7512390;
RA Newman J., Mann N.H., Carr N.G.;
RT "Organization and transcription of the class I phycoerythrin genes of
RL the marine cyanobacterium Synechococcus sp. WH7803.";
RL Plant Mol. Biol. 24:679-683(1994).
CC -! FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
CC FROM THE PHYCOBILIPROTEIN COMPLEX.
CC -! SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -! SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome.
CC -! PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
CC -----
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CC -----
CC EMBL; X72961; CAA51465.1; -
CC PIR; S32642; S32642.
CC PIR; S43779; S43779.
CC HSSP; Q36005; 1B8D.
CC InterPro; IPR001659; Phycobilisome.
CC Pfam; PF00502; Phycobilisome; 1.
CC ProDom; PD000340; Phycobilisome; 1.
CC Phycobilisome; Electron transport; 1.
FT BINDING 82 82 PHYCERYTHROBILIN CHROMOPHORE.
FT BINDING 139 139 PHYCERYTHROBILIN CHROMOPHORE.
SQ SEQUENCE 164 AA; 17853 MW; B443CFD08C859D6A CRC64;

Query Match 100.0%; Score 27; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYVIN 5
DB      157 DYVIN 161

RESULT 4
PHAL_SYNPW
ID PHAL_SYNPW STANDARD; PRT; 164 AA.
AC Q02179;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-phycoerythrin class I alpha chain.
GN CPEA.
OS Synechococcus sp. (strain WH8020).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32052;
RN [1]

```


SEQUENCE FROM N.A.
RX MEDLINE-93144698; PubMed=8425055;
RA de Lorinier R., Walbanks S.M., Glazer A.N.;
RT "Genes of the R-phycoerythrin II locus of marine *Synechococcus* spp.,
and comparison of protein-chromophore interactions in phycocyanins
differing in bilin composition.";
RL Plant Mol. Biol. 21:225-237(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-93123238; PubMed=8419325;
RA Wilbanks S.M., Glazer A.N.;
RT "Rod structure of a phycoerythrin II-containing phycobilisome. I.
Organization and sequence of the gene cluster encoding the major
RT phycobiliprotein rod components in the genome of marine *Synechococcus*
RT sp. WH8020.";
RL J. Biol. Chem. 268:12226-12235(1993).
CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
FROM THE PHYCOBILIPROTEIN COMPLEX.
-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-!- SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome.
-!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
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DR EMBL; M95288; AAA27340.1; -;
DR PIR; G45045; G45045.
DR PIR; S31055; S31055.
DR HSP; O36005; 1B8D.
DR InterPro; IPR001659; Phycobilisome.
DR Pfam; PF00502; Phycobilisome; 1.
DR ProDom; PD000340; Phycobilisome; 1.
KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
FT BINDING 82 82 PHYCOERYTHROBILIN CHROMOPHORE.
FT BINDING 139 139 PHYCOERYTHROBILIN CHROMOPHORE.
SQ SEQUENCE 164 AA; 17860 MW; 7AED0B19EDF5D2C9 CRC64;
Query Match 100.0%; Score 27; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 DYVIN 5
157 DYVIN 161
PHEA GRIMO STANDARD; PRT; 164 AA.
RESULT 5
PHEA GRIMO
ID PHEA GRIMO STANDARD; PRT; 164 AA.
AC O36005;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE R-phycoerythrin alpha chain.
DE Griffithsia monilis.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Ceramiales;
OC Griffithsia.
OX NCBI_TaxID=42003;
RN [1]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RA Ritter S., Hiller R.G., Sharples F.P., Wrench P.M., Welte W.,
RA Diederichs K.;
RT "Crystal structure of a phycoerythrin-containing phycoerythrin at
RT 1.90-A resolution.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases
CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
FROM THE PHYCOBILIPROTEIN COMPLEX.

CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: WITHIN THE THYLAKOID LUMEN. PERIPHERY OF THE
CC RODS OF THE PHYCOBILISOME.
CC -!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
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DR EMBL; Z98528; CAB11029.1; -;
DR PDB; 1B8D; 18-FEB-99.
DR InterPro; IPR001659; Phycobilisome.
DR Pfam; PF00502; Phycobilisome; 1.
DR ProDom; PD000340; Phycobilisome; 1.
KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
FT BINDING 82 82 PHYCOERYTHROBILIN CHROMOPHORE.
FT BINDING 139 139 PHYCOERYTHROBILIN CHROMOPHORE.
SQ SEQUENCE 164 AA; 17669 MW; EFCF110AF760201A CRC64;
Query Match 100.0%; Score 27; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 DYVIN 5
157 DYVIN 161
PHEA RHOVL STANDARD; PRT; 164 AA.
RESULT 6
PHEA RHOVL
ID PHEA RHOVL STANDARD; PRT; 164 AA.
AC Q02036;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE B-phycoerythrin alpha chain.
DE CPEA OR RPEA.
GN Rhodella violacea.
OS Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiales;
OC Rhodella.
OX NCBI_TaxID=2801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93028502; PubMed=1409666;
RA Bernard C., Thomas J.C., Mazel D., Mousseau A., Castets A.M.,
RA Tandeau de Marsac N., Dubacq J.P.;
RT "Characterization of the genes encoding phycoerythrin in the red alga
RT Rhodella violacea: evidence for a splitting of the rpeB gene by an
RT intron.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:9564-9568(1992).
CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
FROM THE PHYCOBILIPROTEIN COMPLEX.
CC -!- SUBUNIT: HETEROPOLYMER OF 6 ALPHA, 6 BETA AND ONE GAMMA CHAINS.
CC -!- SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome.
CC -!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
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DR EMBL; L02188; AAB01576.1; -;
DR PIR; B47207; B47207.
DR HSP; O36005; 1B8D.

```

DR InterPro; IPR001659; Phycobilisome.
DR Pfam; PF00502; Phycobilisome; 1.
DR ProDom; PD000340; Phycobilisome; 1.
KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
KW Chloroplast. 82 82 PHYCOERYTHROBILIN CHROMOPHORE.
FT BINDING 139 139 PHYCOERYTHROBILIN CHROMOPHORE.
FT BINDING 139 139 PHYCOERYTHROBILIN CHROMOPHORE.
SQ SEQUENCE 164 AA; 17696 MW; 6E8494D18B8204FC CRC64;

Query Match 100.0%; Score 27; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
DB 157 DYVIN 161
|||||

RESULT 7
PHEA_SYNP1
ID PHEA_SYNP1 STANDARD; PRT; 164 AA.
P20778:
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DE C-phycoerythrin alpha chain.
GN CPEA OR CPAA.
OS Synechocystis sp. (strain PCC 6701).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1144;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90170840; PubMed=2106507;
RA Anderson L.K., Grossman A.R.;
RT "Structure and light-regulated expression of phycoerythrin genes in
RT wild-type and phycobilisome assembly mutants of Synechocystis sp.
RT strain PCC 6701."
RL J. Bacteriol. 172:1297-1305(1990).
CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome.
CC -!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
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DR EMBL; M33812; AAA27280.1; -
DR PIR; B35127; B35127.
DR HSP; O36005; IB8D.
DR InterPro; IPR001659; Phycobilisome.
DR Pfam; PF00502; Phycobilisome; 1.
DR ProDom; PD000340; Phycobilisome; 1.
KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment.
FT BINDING 82 82 PHYCOERYTHROBILIN CHROMOPHORE.
FT BINDING 139 139 PHYCOERYTHROBILIN CHROMOPHORE.
SQ SEQUENCE 164 AA; 17653 MW; 35CFB8503272E38F CRC64;

Query Match 100.0%; Score 27; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
DB 157 DYVIN 161
|||||

RESULT 8
PHEA_SYNP2

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PHEA_SYNP2
ID PHEA_SYNP2 STANDARD; PRT; 165 AA.
P27646;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-phycoerythrin class II alpha chain.
GN MPEA.
OS Synechococcus sp. (strain WH8020).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32052;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93144698; PubMed=8425055;
RA de Lorimier R., Wilbanks S.M., Glazer A.N.;
RT "Genes of the R-phycoerythrin II locus of marine Synechococcus spp.,
RT and comparison of protein-chromophore interactions in phycocyanins
RT differing in bilin composition."
RL Plant Mol. Biol. 21:225-237(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91236722; PubMed=1903390;
RA Wilbanks S.M., de Lorimier R., Glazer A.N.;
RT "Phycocerythrins of marine unicellular cyanobacteria. III. Sequence of
RT a class II phycoerythrin."
RL J. Biol. Chem. 266:9535-9539(1991).
RN [3]
RP CHROMOPHORES, AND PARTIAL SEQUENCE.
RX MEDLINE=91236720; PubMed=1903388;
RA Ong L.J., Glazer A.N.;
RT "Phycocerythrins of marine unicellular cyanobacteria. I. Bilin types
RT and locations and energy transfer pathways in Synechococcus spp.
RT phycoerythrins."
RL J. Biol. Chem. 266:9515-9527(1991).
CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
CC FROM THE PHYCOBILIPROTEIN COMPLEX.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome.
CC -!- PTM: CONTAINS THREE COVALENTLY LINKED BILIN CHROMOPHORES.
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CC or send an email to license@isb-sib.ch).
DR EMBL; M95288; AAA27333.1; -
DR PIR; A40007; A40007.
DR HSP; O36005; IB8D.
DR InterPro; IPR001659; Phycobilisome.
DR Pfam; PF00502; Phycobilisome; 1.
DR ProDom; PD000340; Phycobilisome; 1.
KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment.
FT BINDING 75 75 PHYCOERYTHROBILIN CHROMOPHORE.
FT BINDING 83 83 PHYCOERYTHROBILIN CHROMOPHORE.
FT BINDING 140 140 PHYCOERYTHROBILIN CHROMOPHORE.
SQ SEQUENCE 165 AA; 17670 MW; B17A9C0BA5D24602 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
DB 158 DYVIN 162
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RESULT 9
PHEA_SYNP2

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Fri Feb 14 15:00:49 2003

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ID PHA2_SYNPE STANDARD; PRT; 165 AA.
AC P37720;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-phycoerythrin class II alpha chain.
GN MPEA.
OS Synechococcus sp. (strain WH8103).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=29410;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=93004492; PubMed=1391782;
RA de Lorimer R., Chen C.-J., Glazer A.N.;
RT "Sequence comparison of two highly homologous phycoerythrins
RL differing in bilin composition."
PL Plant Mol. Biol. 20:353-356(1992).
CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
FROM THE PHYCOBILIPROTEIN COMPLEX.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: Periphery of the rods of the phycobillisome.
CC -!- PTM: CONTAINS THREE COVALENTLY LINKED BILIN CHROMOPHORES.
CC
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CC
DR EMBL; M91809; AAA27322.1; -
DR PIR; S25318; S25318.
DR HSSP; Q36005; LB8P.
DR InterPro; IPR001659; Phycobillisome.
DR Pfam; PF00502; Phycobillisome; 1.
DR ProDom; PD000340; Phycobillisome; 1.
DR Phycobillisome; Electron transport; Photosynthesis; Bile pigment.
KW BINDING 75 PHYCOUROBILIN CHROMOPHORE 1.
FT BINDING 83 83 PHYCOUROBILIN CHROMOPHORE 2.
FT BINDING 140 140 PHYCOUROBILIN CHROMOPHORE 3.
FT BINDING 165 AA; 17729 MW; DBD252CC5DD39B2C CRC64;
SQ SEQUENCE 165 AA; 17729 MW; 17729 MW; Length 165;
Query Match 100.0%; Score 27; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 DYVIN 5
|||||
Db 158 DYVIN 162

RESULT 10
KAD_BACSD STANDARD; PRT; 217 AA.
ID KAD_BACSD Q9WUJ3; Q9WUJ3.
AC P38372; Q9WUJ3; Q9WUJ3.
DT 01-OCT-1994 (Rel. 30, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN ADK OR BH0155.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=9209008; PubMed=10192928;
RA Takami H., Takaki Y., Nakasone K., Hirama C., Inoue A., Horikoshi K.;
RT "Sequence analysis of a 32-kb region including the major ribosomal
RL protein gene clusters from alkaliphilic Bacillus sp. strain C-125.";
RN Biosci. Biotechnol. Biochem. 63:452-455(1999).
[2]

SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kihara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RL halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).
[3]
SEQUENCE OF 1-107 FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=92381482; PubMed=1512566;
RA Kang S.K., Kudo T., Horikoshi K.;
RT "Molecular cloning and characterization of an alkalophilic Bacillus
RL sp. C125 gene homologous to Bacillus subtilis secY.";
J. Gen. Microbiol. 138:1363-1370(1992).
CC -!- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
MAINTENANCE AND CELL GROWTH.
CC -!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC
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DR EMBL; AB017508; BAA75292.1; -
DR EMBL; AP001507; BAB03874.1; -
DR EMBL; D10360; BAA01192.1; -
DR PIR; C44859; C44859.
DR HSSP; P27142; IZIN.
DR InterPro; IPR000850; Adenylate_kin.
DR Pfam; PF00406; adenylatekinase; 1.
DR PRINTS; PR00094; ADENYLTKINASE.
DR ProDom; PD000657; Adenylate_kin; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW Transferase; Kinase; 15 ATP (BY SIMILARITY).
FT NP_BIND 7 4 I -> N (IN REF. 3).
FT CONFLICT 4 4
SQ SEQUENCE 217 AA; 24170 MW; FD5DF854B3BA3592 CRC64;
Query Match 100.0%; Score 27; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 DYVIN 5
|||||
Db 108 DYVIN 112

RESULT 11
KAD_BACSD STANDARD; PRT; 217 AA.
ID KAD_BACSD Q9WUJ3; Q9WUJ3.
AC P16304;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN ADK.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=90292990; PubMed=2113521;
RA Nakamura K., Nakamura A., Takamatsu H., Yoshikawa H., Yamane K.;
RN [2]
```

RT "Cloning and characterization of a Bacillus subtilis gene homologous
 RL to E. coli secY."
 RJ J. Biochem. 107:603-607(1990).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=168 / Marburg;
 RX MEDLINE=96186897; PubMed=8635744;
 RA Suh J.W., Boylan S.A., Oh S.H., Price C.W.;
 RT "Genetic and transcriptional organization of the Bacillus subtilis
 RL spc-alpha region."
 RN Gene 169:17-23(1996).
 RN [3]

RP SEQUENCE OF 1-116 FROM N.A.
 RX MEDLINE=90221911; PubMed=2139212;
 RA Yoshikawa H., Doi R.H.;
 RT "Sequence of the Bacillus subtilis spectinomycin resistance gene
 RL region."
 RN Nucleic Acids Res. 18:1647-1647(1990).
 RN [4]

RP SEQUENCE OF 1-99 FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=90251170; PubMed=2110998;
 RA Suh J.W., Boylan S.A., Thomas S.M., Dolan K.M., Oliver D.B.,
 RT Price C.W.;
 RL "Isolation of a secY homologue from Bacillus subtilis: evidence for a
 common protein export pathway in eubacteria."
 RN Mol. Microbiol. 4:305-314(1990).
 RN [5]

RP SEQUENCE OF 1-20.
 RC STRAIN=168 / IS58;
 RX MEDLINE=97443988; PubMed=9298659;
 RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
 RT Hecker M.;
 RL "First steps from a two-dimensional protein index towards a response-
 RT regulation map for Bacillus subtilis."
 RN Electrophoresis 18:1451-1463(1997).
 RN [6]

CC FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
 CC MAINTENANCE AND CELL GROWTH.

CC SUBUNIT ACTIVITY: ATP + AMP = ADP + ADP.

CC SUBCELLULAR LOCATION: Cytoplasmic.

CC INDUCTION: BY SUPEROXIDE.

CC SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.

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DR EMBL; D00619; BAA00496.1;
 DR EMBL; L47971; AAB06820.1;
 DR EMBL; M31102; AAB59119.1;
 DR EMBL; X51329; CAA35713.1;
 DR EMBL; Z99104; CAB11913.1;
 DR PIR; JS0492; JS0492;
 DR PIR; S08630; S08630;
 DR PIR; S12684; S12684;
 DR HSP; P27142; IZIN.
 DR Subtilist; BG10446; adk.
 DR InterPro; IPR000850; Adenylate_kin.
 DR Pfam; PF00406; adenylatekinase; 1.
 DR PRINTS; P00094; ADENYLKINASE.
 DR ProDom; PD000657; Adenylate_kin; 1.
 DR PROSITE; P500113; ADENYLATE_KINASE; 1.
 KW Transferase; Kinase; ATP-binding; Complete proteome.
 FT NP_BIND 7 15 ATP (BY SIMILARITY).
 SQ SEQUENCE 217 AA; 24119 MW; ECD9ECF4F26A1E90 CRC64;

* Query Match 100.08; Score 27; DB 1; Length 217;
 Best Local Similarity 100.08; Pred. No. 33;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYVIN 5
 Db 108 DYVIN 112

RESULT 12

MTN_BACSU

ID MTN_BACSU

AC 032028;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE MTA/SAH nucleosidase [Includes: 5'-methylthioadenosine nucleosidase

DE (EC 3.2.2.16); S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)].

GN MTN OR PFS.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1423;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RX MEDLINE=98044033; PubMed=9384377;

RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Campiano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,

RA Gusepht G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,

RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Medina N., Levine A., Liu H., Masuda S., Maestl D., Lazarevic V.,

RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,

RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

RA Tosato V., Uchiyama S., Vandenberg M., Vannier F., Vassarotti A.,

RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenger T.,

RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

RT subtilis".

RL Nature 390:249-256(1997).

CC FUNCTION: RESPONSIBLE FOR CLEAVAGE OF THE GLYCOSIDIC BOND IN BOTH

CC 5'-METHYLTHIOADENOSINE (MTA) AND S-ADENOSYLHOMOCYSTEINE (SAH) (BY

CC SIMILARITY).

CC CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenine +

CC S-D-ribosyl-L-homocysteine.

CC CATALYTIC ACTIVITY: Methylthioadenosine + H(2)O = adenine + 5-

CC methylthio-D-ribose.

CC SIMILARITY: BELONGS TO THE MTN FAMILY.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; Z99117; CAB14669.1; .

DR Subtilist; BGI3800; mtm.
 DR InterPro; IPR000845; PNP_UDP.
 DR Pfam; PF01048; PNP_UDP_1; 1.
 DR ProDom; PD003928; PNP_UDP; 1.
 KW Hydrolase; Multifunctional enzyme; Complete proteome.
 SQ SEQUENCE 231 AA; 25264 MW; 7F6B8BC8EDA1E728 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 231;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5
 |||||
 Db 69 DYVIN 73

RESULT 13
 ANFD_HELGE STANDARD; PRT; 280 AA.
 O68955;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Nitrogenase iron-iron protein alpha chain (EC 1.18.6.1) (Nitrogenase
 component I) (Dinitrogenase 3 alpha subunit) (Fragment).
 GN ANFD.
 OS Hellobacterium gestii.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Hellobacteriaceae;
 OC Hellobacterium.
 OX NCBI_TaxID=2699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Loveless T.M., Bishop P.E.;
 RT "Identification of genes unique to Mo-independent nitrogenase systems
 in diverse diazotrophs.";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THE KEY ENZYMIC REACTIONS IN NITROGEN FIXATION ARE
 CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
 IRON PROTEIN (COMPONENT 2) AND A COMPONENT 1 WHICH IS EITHER A
 MOLYBDENUM-IRON PROTEIN, A VANADIUM-IRON, OR AN IRON-IRON PROTEIN.
 CC -!- CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 ATP
 CC = 8 oxidized ferredoxin + 2 NH(3) + 16 ADP + 16 phosphate.
 CC -!- COFACTOR: IRON-SULFUR (BY SIMILARITY).
 CC -!- SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO DELTA CHAINS (BY
 SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF058785; AAC14342.1; -;
 CC HSSP; P00467; 1MIO.
 CC InterPro; IPR000318; Nitrogense_comp1.
 CC InterPro; IPR000510; Oxred_nitrogensel.
 CC Pfam; PF00148; oxidored_nitro; 1.
 CC TIGRFAMs; TIGR01284; alt_nitrog_alph; 1.
 CC PROSITE; PS00090; NITROGENASE_1_2; 1.
 CC PROSITE; PS00699; NITROGENASE_1_1; 1.
 KW Oxidoreductase; Nitrogen fixation; Iron-sulfur.
 FT NON_TER 1 1
 FT NON_TER 280 280
 SQ SEQUENCE 280 AA; 31772 MW; CDF253376AF1056A1 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 280;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5

Db 158 DYVIN 162
 |||||
 RESULT 14
 ADH_SULSO STANDARD; PRT; 347 AA.
 ID ADH_SULSO
 AC P39462; O74076;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE NAD-dependent alcohol dehydrogenase (EC 1.1.1.1).
 GN ADH OR SSO2536.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=93099126; PubMed=1463738;
 RA Amendola S., Raia C.A., Caruso C., Camardella L., D'Auria S.,
 de Rosa M., Rossi M.;
 RT "Thermostable NAD(+)-dependent alcohol dehydrogenase from Sulfolobus
 solfataricus: gene and protein sequence determination and
 relationship to other alcohol dehydrogenases.";
 RL Biochemistry 31:12514-12523(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 35092 / DSM 1617 / P2;
 RA Aravalli R.N.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=21322296; PubMed=11427726;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 Awayez M.A., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,
 De Moors A., Frausto G., Fletcher C., Gordon P.M.K.,
 Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 Garrett R.A., Ragan M.A., Sensesen C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 CC -!- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 NADH.
 CC -!- COFACTOR: ZINC; BINDS 4 ZINC IONS PER DIMER.
 CC -!- SUBUNIT: HOMODIMER AND HOMOTETRAMER.
 CC -!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 FAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; S51211; AAB24546.1; -;
 CC EMBL; AJ010590; CAA09258.1; -;
 CC EMBL; AE006850; AAK42665.1; -;
 CC PIR; A44245; A44245.
 CC InterPro; IPR002328; ADH_zinc.
 CC InterPro; IPR002085; Adh_zn_family.
 CC InterPro; IPR000051; SAM_bind.
 CC Pfam; PF00107; adh_zinc; 1.
 CC PROSITE; PS00059; ADH_ZINC; 1.
 KW Oxidoreductase; Zinc; NAD; Methylation; Complete proteome.
 FT MOD_RES 11 11
 FT MOD_RES 213 213 METHYLATION.
 FT METAL 38 38 ZINC (CATALYTIC) (BY SIMILARITY).
 FT

```

FT METAL 68 68 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 98 98 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 101 101 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 104 104 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 112 112 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 154 154 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 347 AA; 37568 MW; 755848A249D4F4A2 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 218 DYVIN 222

RESULT 15
ADH_SULSR STANDARD; PRT; 347 AA.
AC P50381;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DE NAD-dependent alcohol dehydrogenase (EC 1.1.1.1).
GN ADH.
OS Sulfolobus sp. (strain RC3).
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=165757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96125263; PubMed=8550434;
RA Cannio R., Fiorentino G., Carpinelli P., Rossi M., Bartolucci S.;
RT "Cloning and overexpression in Escherichia coli of the genes encoding
RL NAD-dependent alcohol dehydrogenase from two Sulfolobus species.";
RL J. Bacteriol. 178:301-305(1996).
CC -!- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
CC NADH.
CC -!- COFACTOR: ZINC; BINDS 4 ZINC IONS PER DIMER.
CC -!- SUBUNIT: HOMODIMER AND HOMOTETRAMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC -----
DR EMBL; Z47543; CAA87591.1; -.
DR InterPro; IPR002328; ADH_zinc.
DR InterPro; IPR002085; Adh_zn_family.
DR InterPro; IPR000051; SAM_bind.
DR Pfam; PF00107; adh_zinc; 1.
DR PROSITE; PS00059; ADH_ZINC; 1.
KW Oxidoreductase; Zinc; NAD; Methylation.
FT MOD_RES 11 11 METHYLATION (BY SIMILARITY).
FT MOD_RES 213 213 METHYLATION (BY SIMILARITY).
FT METAL 38 38 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 68 68 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 98 98 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 101 101 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 104 104 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 112 112 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 154 154 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 347 AA; 37583 MW; 55D3C003792DE60D CRC64;

Query Match 100.0%; Score 27; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DYVIN 5
Db 218 DYVIN 222

Search completed: February 14, 2003, 11:16:19
Job time : 3.58065 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:10:17 ; Search time 10.4032 Seconds
(without alignments)
99.030 Million cell updates/sec

Title: US-09-701-001B-1

Perfect score: 27

Sequence: 1 DYVIN 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 671580 seqs, 206047115 residues 671580

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_virus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	27	100.0	82	2 Q9L4G6	Q9L4G6 streptococ
2	27	100.0	113	5 Q9VEV5	Q9VEV5 drosophila
3	27	100.0	149	5 Q9V965	Q9V965 drosophila
4	27	100.0	185	12 Q9EMY1	Q9EMY1 amsacta moo
5	27	100.0	197	17 Q8U241	Q8U241 pyrococcus
6	27	100.0	231	8 Q9MJ64	Q9MJ64 physarum po
7	27	100.0	258	11 Q9R282	Q9R282 mus musculu
8	27	100.0	259	16 Q9ROW0	Q9ROW0 neisseria m
9	27	100.0	298	16 Q98160	Q98160 rhizobium l
10	27	100.0	299	16 Q98RF0	Q98RF0 mycoplasma
11	27	100.0	303	16 Q9CG74	Q9CG74 lactococcus
12	27	100.0	341	16 Q9HV17	Q9HV17 pseudomonas
13	27	100.0	345	16 Q9K724	Q9K724 bacillus ha
14	27	100.0	347	17 Q96XE0	Q96XE0 sulfolobus
15	27	100.0	348	17 Q58389	Q58389 pyrococcus
16	27	100.0	348	17 Q9UYX0	Q9UYX0 pyrococcus

17	27	100.0	348	17 Q8U259	Q8U259 pyrococcus
18	27	100.0	349	4 Q9UQ51	Q9UQ51 homo sapien
19	27	100.0	353	16 Q9A6L1	Q9A6L1 caulobacter
20	27	100.0	353	16 Q8YZN1	Q8YZN1 anabaena sp
21	27	100.0	357	2 Q85768	Q85768 legionella
22	27	100.0	359	13 Q9YH97	Q9YH97 tetraodon f
23	27	100.0	359	13 Q9YH96	Q9YH96 fugu rubrip
24	27	100.0	360	13 Q9YGC9	Q9YGC9 brachydanio
25	27	100.0	364	16 Q9K985	Q9K985 bacillus ha
26	27	100.0	376	16 Q99TD9	Q99TD9 staphylococ
27	27	100.0	380	2 Q8RN27	Q8RN27 campylobact
28	27	100.0	380	16 Q9PMB8	Q9PMB8 campylobact
29	27	100.0	386	16 Q9HZV8	Q9HZV8 pseudomonas
30	27	100.0	399	5 Q9NC97	Q9NC97 trypanosoma
31	27	100.0	407	16 Q96831	Q96831 mycobacteri
32	27	100.0	420	16 Q8XXU3	Q8XXU3 ralstonia s
33	27	100.0	423	16 Q9CNX7	Q9CNX7 pasteurella
34	27	100.0	431	16 Q9S2H5	Q9S2H5 streptomyce
35	27	100.0	444	16 Q9A1M4	Q9A1M4 streptococ
36	27	100.0	464	5 Q01607	Q01607 caenorhabdi
37	27	100.0	488	17 Q58017	Q58017 pyrococcus
38	27	100.0	488	17 Q8WZP5	Q8WZP5 pyrococcus
39	27	100.0	492	16 Q8UHV4	Q8UHV4 agrobacteri
40	27	100.0	520	5 Q17175	Q17175 caenorhabdi
41	27	100.0	543	5 Q9V7R9	Q9V7R9 drosophila
42	27	100.0	584	2 Q45397	Q45397 prevotella
43	27	100.0	593	17 Q97BL5	Q97BL5 thermoplasm
44	27	100.0	610	16 Q86712	Q86712 streptomyce
45	27	100.0	616	5 Q9V7P8	Q9V7P8 drosophila

ALIGNMENTS

RESULT 1

ID	Q9L4G6	PRELIMINARY;	PRT;	82 AA.
AC	Q9L4G6;			
DT	01-OCT-2000 (Tremblrel. 15, Created)			
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE	Xis (Excisionase).			
GN	XIS.			
OS	Streptococcus thermophilus.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;			
OC	Streptococcaceae; Streptococcus.			
OX	NCBI_TaxID=1308;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CNRZ368;			
RC	MEDLINE=20208895; PubMed=10742276;			
RA	Burris V., Roussel Y., Decaris B., Guedon G.;			
RA	"Characterization of a novel integrative element, ICEstl, in the			
RT	lactic acid bacterium streptococcus thermophilus.;"			
RL	Appl. Environ. Microbiol. 66:1749-1753(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CNRZ368;			
RC	MEDLINE=95379495; PubMed=76511138;			
RA	Guedon G., Bourgoin F., Pebay M., Roussel Y., Colmin C., Simonet J.M.,			
RA	Decaris B.;			
RT	"Characterization and distribution of two insertion sequences, IS1191			
RT	and iso-IS981, in Streptococcus thermophilus: does intergeneric			
RT	transfer of insertion sequences occur in lactic acid bacteria co-			
RT	cultures?";			
RL	Mol. Microbiol. 16:69-78(1995).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CNRZ368;			
RC	MEDLINE=97286550; PubMed=9141697;			
RA	Roussel Y., Bourgoin F., Guedon G., Pebay M., Decaris B.;			
RT	"Analysis of the genetic polymorphism between three Streptococcus			
RT	thermophilus strains by comparing their physical and genetic			

RT organization. ";
 DR EMBL; AJ243106; CAB70621.1; -;
 DR EMBL; AJ278471; CAC67553.1; -;
 SQ SEQUENCE 82 AA; 9901 MW; 1681678702142DFD CRC64;

Query Match 100.0%; Score 27; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||||
 Db 49 DYVIN 53

RESULT 2

Q9VEV5 PRELIMINARY; PRT; 113 AA.
 AC Q9VEV5
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 CG10406 protein.
 MRPS33 OR CG10406.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003713; AAF55312.1; -;
 DR FlyBase; FBgn0038426; mrps33.

SQ SEQUENCE 113 AA; 13685 MW; 1943154BABDB2926 CRC64;

Query Match 100.0%; Score 27; DB 5; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||||
 Db 54 DYVIN 58

RESULT 3

Q9V965 PRELIMINARY; PRT; 149 AA.
 AC Q9V965
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE CG13437 protein.
 GN CG13437
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003791; AAF57432.1; -;
 DR FlyBase; FBgn0034541; CG13437.
 SQ SEQUENCE 149 AA; 17627 MW; 095FFFAA04D7EA12F CRC64;

Query Match 100.0%; Score 27; DB 5; Length 149;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
11111
Db 114 DYVIN 118

RESULT 4

Q9EMV1 PRELIMINARY; PRT; 185 AA.

AC Q9EMV1; (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE AMV068.
GN AMV068.

OS Anasacta moorei entomopoxvirus (AmEPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
NCBI_TaxID=28321;

QY 1
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20396580; PubMed=10936094;
RA Bowden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,
Moyer R.W.;
RT "Complete Genomic Sequence of the Anasacta moorei Entomopoxvirus;
RT Analysis and Comparison with Other Poxviruses.";
RL Virology 274:120-139(2000).
RN [2]

RP SEQUENCE FROM N.A.
RA Bowden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,
Moyer R.W.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF250284; AAG02774.1; -;
SQ SEQUENCE 185 AA; 21994 MW; FD9F960A83DFF033 CRC64;

Query Match 100.0%; Score 27; DB 12; Length 185;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
11111
Db 71 DYVIN 75

RESULT 5

Q8U241 PRELIMINARY; PRT; 197 AA.

AC Q8U241; (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein PF1009.
GN PF1009.

OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;

QY 1
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010212; AAL81133.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 197 AA; 23432 MW; 516CB4985B1E083B CRC64;

Query Match 100.0%; Score 27; DB 17; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5

11111
Db 18 DYVIN 22

RESULT 6

Q9MJ64 PRELIMINARY; PRT; 231 AA.

AC Q9MJ64; (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE ORF18.

OS Physarum polycephalum (Slime mold).
OG Mitochondrion.
OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
OC Physarum.

OX NCBI_TaxID=5791;

QY 1
RN [1]
RP SEQUENCE FROM N.A.
RX Takano H.; (MAY-1999) to the EMBL/GenBank/DBJ databases.
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=21080535; PubMed=11212908;
RA Takano H., Abe T., Sakurai R., Moriyama Y., Miyazawa Y., Nozaki H.,
Kawano S., Sasaki N., Kuroiwa T.;
RT "The complete DNA sequence of the mitochondrial genome of Physarum
polycephalum.";
RL Mol. Gen. Genet. 264:539-545(2001).
DR EMBL; AB027295; BAB08098.1; -;
KW Mitochondrion.
SQ SEQUENCE 231 AA; 25949 MW; 0FD9ECD3A2058C0C CRC64;

Query Match 100.0%; Score 27; DB 8; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
11111
Db 154 DYVIN 158

RESULT 7

Q9R282 PRELIMINARY; PRT; 258 AA.

AC Q9R282; (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Spermine synthase (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

QY 1
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SVJ;
MEDLINE=21106296; PubMed=11160858;

RA Korhonen V.P., Niiranen K., Halmekyto M., Pietila M., Diegelman P.,
Parkkinen J.J., Eloranta T., Porter C.W., Alhonen L., Janne J.;
RT "Spermine Deficiency Resulting from Targeted Disruption of the
Spermine Synthase Gene in Embryonic Stem Cells Leads to Enhanced
Sensitivity to Antiproliferative Drugs.";
RL Mol. Pharmacol. 59:231-238(2001).
DR EMBL; AF136179; AAD33057.1; -;

DR InterPro; IPR001045; Sprmine_synthase.
DR Pfam; PF01564; Spermine_synth; 1.
DR PROSITE; PS01330; SPERMIDINE_SYNTHASE; 1.
FT NON_TER 1
FT NON_TER 258
SQ SEQUENCE 258 AA; 29165 MW; 742A778011ACC8D2 CRC64;

Query Match 100.0%; Score 27; DB 11; Length 258;

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Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 214 DYVIN 218

RESULT 8
Q9ROWO
ID Q9ROWO PRELIMINARY; PRT; 259 AA.
AC Q9ROWO
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TOU3.
DE TOU3 OR NNA2036.
GN Neisseria meningitidis (serogroup A).
OS Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OC NCBI_TaxID=65699;
OX [1]
RN [1]
SEQUENCE FROM N.A.
STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491.";
RL Nature 404:502-506(2000).
DR EMBL; AF058689; AAF06687.1; -
DR EMBL; AL162757; CAB85255.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 259 AA; 29564 MW; FC2AD5234C6E4CBE CRC64;

Query Match 100.0%; Score 27; DB 16; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 78 DYVIN 82

RESULT 9
Q98160
ID Q98160 PRELIMINARY; PRT; 298 AA.
AC Q98160
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Probable transcriptional regulator.
GN MLL2551.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
SEQUENCE FROM N.A.
STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003000; BAB49656.1; -

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DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 298 AA; 33459 MW; 2D9176927BEB7DE3 CRC64;

Query Match 100.0%; Score 27; DB 16; Length 298;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 245 DYVIN 249

RESULT 10
Q98RF0
ID Q98RF0 PRELIMINARY; PRT; 299 AA.
AC Q98RF0
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Hypothetical protein MYPUL_0590.
GN MYPUL_0590.
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN=UAB CTIP;
RX MEDLINE=21267165; PubMed=11353084;
RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Mosser I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis.";
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL; AL445563; CAC13232.1; -
DR MYPUL1st; MYPUL_0590; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 299 AA; 35162 MW; F932B224FC7CC801 CRC64;

Query Match 100.0%; Score 27; DB 16; Length 299;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 73 DYVIN 77

RESULT 11
Q9CG74
ID Q9CG74 PRELIMINARY; PRT; 303 AA.
AC Q9CG74
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE LysR family transcriptional regulator.
GN RLRA OR LL1236.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Manger S., Jaillon O., Malarre K.,

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RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium *Lactococcus*
 RT *lactis* ssp. *lactis* IIL1403.";
 RL Genome Res. 11:731-753(2001).
 CC 1- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
 DR EMBL: AE006355; RAK05334.1; -;
 DR InterPro: IPR000847; HTH_LysR.
 DR InterPro: IPR005119; LysR_subst.
 DR Pfam: PF00126; HTH_1; 1.
 DR Pfam: PF03466; LysR_substrate; 1.
 DR PRINTS: PR00039; HTHLYSR.
 DR PROSITE: PS00044; HTH_LYSR_FAMILY; UNKNOWN1.
 DR DNA-binding; Transcription regulation; Complete proteome.
 KW DNA-binding; Transcription regulation; Complete proteome.
 SQ SEQUENCE 303 AA; 34906 MW; 79FF10A56FC8983 CRC64;

Query Match 100.0%; Score 27; DB 16; Length 303;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||||
 Db 209 DYVIN 213

RESULT 12

Q9HYI7 PRELIMINARY; PRT; 341 AA.
 AC Q9HYI7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Leucine dehydrogenase.
 GN LDH OR PA3418.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 Raizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
 opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 DR EMBL: AE004763; AAC06806.1; -;
 DR InterPro: IPR001625; GLFV_Dh.
 DR InterPro: IPR000205; NAD_binding.
 DR Pfam: PF00208; GLFV_dehydrog; 1.
 DR Pfam: PF02812; GLFV_dehydrog_N; 1.
 DR PRINTS: PR00082; GLFV_DHGRNASE.
 KW Complete proteome.
 SQ SEQUENCE 341 AA; 35633 MW; ECCB810C13BF0B40 CRC64;

Query Match 100.0%; Score 27; DB 16; Length 341;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||||
 Db 277 DYVIN 281

RESULT 13

Q9K724 PRELIMINARY; PRT; 345 AA.
 AC Q9K724;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein BH3213.
 GN BH3213.
 OS *Bacillus halodurans*.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 "Complete genome sequence of the alkaliphilic bacterium *Bacillus*
 RT *halodurans* and genomic sequence comparison with *Bacillus subtilis*.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL: AP001518; BAB06932.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 345 AA; 38740 MW; 938F7707056F598E CRC64;

Query Match 100.0%; Score 27; DB 16; Length 345;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||||
 Db 144 DYVIN 148

RESULT 14

Q96XE0 PRELIMINARY; PRT; 347 AA.
 AC Q96XE0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Putative alcohol dehydrogenase.
 GN S72577.
 OS *Sulfolobus tokodaii*.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX PubMed=11572479;
 RA Kwarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 "Complete genome sequence of an aerobic thermoacidophilic
 RT *Crenarchaeon*, *Sulfolobus tokodaii* strain 7.";
 RL DNA Res. 8:123-140(2001).
 DR EMBL: AP000950; BAB67688.1; -;
 DR InterPro: IPR002328; ADH_zinc.
 DR InterPro: IPR002085; Adh_zn_family.
 DR InterPro: IPR000051; SAM_bind.
 DR Pfam: PF00107; adh_zinc; 1.
 DR PROSITE: PS00059; ADH_ZINC; UNKNOWN1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 347 AA; 37569 MW; 46059B8AE2382DF0 CRC64;

Query Match 100.0%; Score 27; DB 17; Length 347;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
 |||||
 Db 218 DYVIN 222

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RESULT 15
O58389 ID O58389 PRELIMINARY; PRT; 348 AA.
AC O58389; 1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE 348AA long hypothetical dehydrogenase.
GN Ph0655.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=96344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:55-76(1998).
CC -!- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).
DR EMBL: AP000003; BAA29746.1; -.
DR HSSP: P07846; ISDG.
DR InterPro: IPR002328; ADH_zinc.
DR InterPro: IPR002085; Adh_zn_family.
DR InterPro: IPR004627; Tdh.
DR Pfam: PF00107; adh_zinc; 1.
DR TIGRFAMs: TIGR00692; tdh; 1.
DR PROSITE: PS00059; ADH_ZINC; 1.
KW Oxidoreductase; Zinc; Complete proteome.
SQ SEQUENCE 348 AA; 37785 MW; 313F368AE83F793E CRC64;

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Query Match      100.0%; Score 27; DB 17; Length 348;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DYVIN 5
DB 214 DYVIN 218

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Search completed: February 14, 2003, 11:18:36
time : 12.5699 secs

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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:04:17 ; Search time 46.0645 Seconds
(without alignments)
49.176 Million cell updates/sec

Title: US-09-701-001b-2
Perfect score: 94
Sequence: 1 E1YPGSGAYNEMFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
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- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	17	AAV59257	Antibody 4H5 H cha
2	94	100.0	17	AAV51134	Murine CD4/CD34 re
3	94	100.0	110	AAV59262	Antibody 4H5 H cha
4	94	100.0	110	AAV51139	Murine derived pro
5	94	100.0	118	AAV59266	Antibody 4H5 H cha
6	94	100.0	118	AAV51143	Murine derived pro
7	94	100.0	118	AAV51145	Murine derived pro
8	94	100.0	305	AAV59264	Antibody 4H5 H cha
9	94	100.0	305	AAV59265	Antibody 4H5 L cha
10	94	100.0	305	AAV51141	Murine derived pro

11	94	100.0	305	21	AAV51142	Murine derived pro
12	88	93.6	119	21	AAV51264	Monoclonal antibod
13	88	93.6	137	14	AAV32124	Anti-CD4 antibody
14	81	86.2	121	18	AAV07437	Anti-DNA antibody
15	76	80.9	123	16	AAV07977	Anti-EGFR antibody
16	73	77.7	113	18	AAV04591	Anti-DNA antibody
17	73	77.7	248	20	AAV17960	Mouse scfV fragmen
18	73	77.7	248	20	AAV17965	Mouse scfV fragmen
19	72	76.6	116	17	AAV03742	Murine monoclonal
20	71	75.5	355	18	AAV35133	R. pipiens recombi
21	70	74.5	242	20	AAV17959	Mouse scfV fragmen
22	70	74.5	242	20	AAV17961	Mouse scfV fragmen
23	70	74.5	251	20	AAV17958	Mouse scfV fragmen
24	70	74.5	251	20	AAV17962	Mouse scfV fragmen
25	70	74.5	507	23	AAV72858	8G7C10x4-7 bispeci
26	70	74.5	510	23	AAV72859	6E5A7x4-7 bispeci
27	70	74.5	510	23	AAV72860	Human p53 tetramer
28	70	74.5	532	21	AAV78328	Bispecific anti-ze
29	68	72.3	91	18	AAV18276	PrP 24 antibody fr
30	68	72.3	91	18	AAV18267	PrP 81 heavy chain
31	68	72.3	91	20	AAV85906	PrP 81 heavy chain
32	68	72.3	91	20	AAV85914	Amino acid sequenc
33	68	72.3	91	22	AAV65858	Anti-PrP antibody
34	68	72.3	91	22	AAV65866	Anti-PrP antibody
35	68	72.3	91	23	ABP51792	Anti-prion protein
36	68	72.3	91	23	ABP51800	Anti-prion protein
37	68	72.3	92	18	AAV18277	PrP 26 antibody fr
38	68	72.3	92	18	AAV18284	PrP 39 antibody fr
39	68	72.3	92	20	AAV85921	Amino acid sequenc
40	68	72.3	92	20	AAV85915	Amino acid sequenc
41	68	72.3	92	22	AAV65867	Anti-PrP antibody
42	68	72.3	92	22	AAV65873	Anti-PrP antibody
43	68	72.3	92	23	ABP51801	Anti-prion protein
44	68	72.3	92	23	ABP51807	Anti-prion protein
45	68	72.3	95	18	AAV18285	PrP 40 antibody fr

ALIGNMENTS

RESULT 1
AAV59257
ID AAY59257 standard; peptide; 17 AA.
XX AAY59257;
XX AC
XX DT 17-APR-2000 (first entry)
XX Antibody 4H5 H chain variable region CDR2 fragment.
DE CD4 antigen; anti-human; antibody; 4H5; drug; CDR;
KW complementarity determining region.
XX Mus sp.
XX JP11332563-A.
XX 07-DEC-1999.
XX 26-MAY-1998; 98JP-0163034.
XX 26-MAY-1998; 98JP-0163034.
XX (ASAH) ASAH KASEI KOGYO KK.
XX WPI; 2000-091351/08.
XX An antibody and the nucleic acid coding the antibody -
XX Claim 1; Page 14; 25pp; Japanese.
XX The invention provides an antibody having affinity to CD4 antigen. The
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and

CC application for drugs. It is highly safe in human dose. Sequences
 CC AAY59256-58 represent the complementarity determining region (CDR)-1,
 CC CDR-2 and CDR-3 fragments in the H chain variable region of the
 CC antibody 4H5 respectively.
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 94; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYPGSGSAYYNEMFKG 17
 |||||
 Db 1 EYPGSGSAYYNEMFKG 17

RESULT 2
 AAY51134
 ID AAY51134 standard; Protein; 17 AA.
 XX
 AC AAY51134;
 DT 31-MAR-2000 (first entry)

DE Murine CD4/CD34 recognizing antibody heavy chain CDR-2 region #1.

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; complementarity determining region;
 KW CDR-2; heavy chain; murine.
 XX

OS Mus sp.
 XX
 PN WO9961629-A1.
 XX
 PD 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711. - *pat priority for instant*
 XX 25-MAY-1998; 98JP-0159957.
 PR 26-MAY-1998; 98JP-0163023.

XX (ASAH) KASEI KOGYO KK.
 PA (ASAH) ASAHI MEDICAL CO LTD.

PI Ono M, Soka T, Morimoto I, Miyamura K;

XX WPI; 2000-086720/07.

XX Devices containing antibodies recognising CD4 or CD34 and their use for
 the separation of CD4 or CD34 positive cells -

PS Claim 3; Page 76; 11ipp; Japanese.

XX This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived complementarity determining
 CC region CDR-2 protein fragment which is used to illustrate the method of
 CC the invention.
 XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 94; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYPGSGSAYYNEMFKG 17

Db 1 EYPGSGSAYYNEMFKG 17
 |||||

RESULT 3
 AAY59262
 ID AAY59262 standard; protein; 110 AA.
 XX
 AC AAY59262;
 DT 17-APR-2000 (first entry)
 XX
 DE Antibody 4H5 H chain variable region.
 XX
 KW CD4 antigen; anti-human; antibody; 4H5; drug.
 XX
 OS Mus sp.

XX JPI1332563-A.
 PN 07-DEC-1999.
 PD 26-MAY-1998; 98JP-0163034.
 PF 26-MAY-1998; 98JP-0163034.
 PR (ASAH) KASEI KOGYO KK.

XX WPI; 2000-091351/08.
 DR N-PSDB; AAZ58661.

XX An antibody and the nucleic acid coding the antibody -
 XX
 PS Claim 5; Page 15; 25pp; Japanese.
 XX
 CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the H chain variable region of the antibody 4H5.
 XX
 SQ Sequence 110 AA;

Query Match 100.0%; Score 94; DB 21; Length 110;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYPGSGSAYYNEMFKG 17
 |||||
 Db 42 EYPGSGSAYYNEMFKG 58

RESULT 4
 AAY51139
 ID AAY51139 standard; Protein; 110 AA.
 XX
 AC AAY51139;

XX 31-MAR-2000 (first entry)
 DT
 XX Murine derived protein fragment #1.
 DE

XX Cluster differentiation; cell separation; antibody; CD4; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 XX
 OS Mus sp.

XX WO9961629-A1.
 PN 02-DEC-1999.
 PD 24-MAY-1999; 99WO-JP02711. - *pat priority for instant*

PR 25-MAY-1998; 98JP-0159957.
PR 26-MAY-1998; 98JP-0163023.
XX (ASAH) ASahi KASEI KOGYO KK.
PA (ASAH) ASahi MEDICAL CO LTD.
XX
PI Ono M, Soka T, Morimoto I, Miyamura K;
XX WPI: 2000-086720/07.
DR N-PSDB; AA244203.
XX
XX
PT Devices containing antibodies recognising CD4 or CD34 and their use for
PT the separation of CD4 or CD34 positive cells -
XX
XX Claim 22; Page 78; 111pp; Japanese.
XX
XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for
XX the collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal
XX compositions for the treatment of HIV infection and autoimmune diseases.
XX This sequence represents a murine derived protein fragment which is used
XX to illustrate the method of the invention.
XX
SQ Sequence 110 AA;
Query Match 100.0%; Score 94; DB 21; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIYPGSGSAYYNEMFKG 17
DB 42 EIYPGSGSAYYNEMFKG 58
RESULT 5
AA59266
ID AA59266 standard; protein; 118 AA.
XX
XX AA59266;
XX
XX 17-APR-2000 (first entry)
XX
XX Antibody 4H5 H chain fragment.
XX
XX CD4 antigen; anti-human; antibody; 4H5; drug.
XX
XX Mus sp.
XX JP11332563-A.
XX
XX 07-DEC-1999.
XX
XX 26-MAY-1998; 98JP-0163034.
XX
XX 26-MAY-1998; 98JP-0163034.
XX
XX (ASAH) ASahi KASEI KOGYO KK.
XX
XX WPI: 2000-091351/08.
XX N-PSDB; AA258689.
XX
XX An antibody and the nucleic acid coding the antibody -
PT
XX
XX Disclosure; Page 22; 25pp; Japanese.
XX
XX The invention provides an antibody having affinity to CD4 antigen. The
XX anti-human CD4 antibody 4H5 is used for the detection of antigen and
XX application for drugs. It is highly safe in human dose. The present
XX sequence represents a H chain fragment of the antibody 4H5.

XX Sequence 118 AA;
SQ
Query Match 100.0%; Score 94; DB 21; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIYPGSGSAYYNEMFKG 17
DB 50 EIYPGSGSAYYNEMFKG 66
RESULT 6
AA51143
ID AA51143 standard; Protein; 118 AA.
XX
XX AA51143;
XX
XX 31-MAR-2000 (first entry)
XX
XX Murine derived protein fragment #5.
XX
XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
XX hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
XX HIV infection; autoimmune disease; murine.
XX
XX Mus sp.
XX
XX WO9961629-A1.
XX
XX 02-DEC-1999.
XX
XX 24-MAY-1999; 99WO-JP02711.
XX
XX 25-MAY-1998; 98JP-0159957.
XX 26-MAY-1998; 98JP-0163023.
XX
XX (ASAH) ASahi KASEI KOGYO KK.
XX (ASAH) ASahi MEDICAL CO LTD.
XX
XX Ono M, Soka T, Morimoto I, Miyamura K;
XX
XX WPI: 2000-086720/07.
XX
XX Devices containing antibodies recognising CD4 or CD34 and their use for
XX the separation of CD4 or CD34 positive cells -
XX
XX Disclosure; Page 94-95; 111pp; Japanese.
XX
XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for
XX the collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal
XX compositions for the treatment of HIV infection and autoimmune diseases.
XX This sequence represents a murine derived protein fragment which is used
XX to illustrate the method of the invention.
XX
XX Sequence 118 AA;
SQ
Query Match 100.0%; Score 94; DB 21; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIYPGSGSAYYNEMFKG 17
DB 50 EIYPGSGSAYYNEMFKG 66
RESULT 7
AA51145

ID AAY51145 standard; Protein; 118 AA.
 XX AC AAY51145;
 XX DT 31-MAR-2000 (first entry)
 XX DE Murine derived protein fragment #7.
 XX DE Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hemopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 XX OS Mus sp.
 XX PN WO9961629-A1.
 XX PD 02-DEC-1999.
 XX PF 24-MAY-1999; 99WO-JP02711.
 XX PR 25-MAY-1998; 98JP-0159957.
 XX PR 26-MAY-1998; 98JP-0163023.
 XX PR (ASAH) ASahi KASEI KOGYO KK.
 XX PA (ASAH) ASahi MEDICAL CO LTD.
 XX PI Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI; 2000-086720/07.
 XX DR N-PSDB; AAZ44231.
 XX PT Devices containing antibodies recognising CD4 or CD34 and their use for
 XX the separation of CD4 or CD34 positive cells -
 XX PS Disclosure; Page 96-97; 11pp; Japanese.
 XX CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 XX SQ Sequence 118 AA;

Query Match 100.0%; Score 94; DB 21; Length 118;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYPGSGSAYYNEMFKG 17
 ||||||||||||||||
 Db 50 EYPGSGSAYYNEMFKG 66

RESULT 8
 AAY59264
 ID AAY59264 standard; protein; 305 AA.
 XX AC AAY59264;

XX DT 17-APR-2000 (first entry)
 XX DE Antibody 4H5 H chain sequence.
 XX KW CD4 antigen; anti-human; antibody; 4H5; drug.
 XX OS Mus sp.
 XX PN JP11332563-A.

XX PD 07-DEC-1999.
 XX PF 26-MAY-1998; 98JP-0163034.
 XX PR 26-MAY-1998; 98JP-0163034.
 XX PR (ASAH) ASahi KASEI KOGYO KK.
 XX PA WPI; 2000-091351/08.
 XX DR N-PSDB; AAZ58663.
 XX PT An antibody and the nucleic acid coding the antibody -
 XX PS Disclosure; Page 16-17; 25pp; Japanese.
 XX CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the H chain sequence of the antibody 4H5.
 XX SQ Sequence 305 AA;

Query Match 100.0%; Score 94; DB 21; Length 305;
 Best Local Similarity 100.0%; Pred. No. 9.4e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYPGSGSAYYNEMFKG 17
 ||||||||||||||||
 Db 198 EYPGSGSAYYNEMFKG 214

RESULT 9
 AAY59265
 ID AAY59265 standard; protein; 305 AA.
 XX AC AAY59265;

XX DT 17-APR-2000 (first entry)
 XX DE Antibody 4H5 L chain sequence.
 XX KW CD4 antigen; anti-human; antibody; 4H5; drug.
 XX OS Mus sp.
 XX PN JP11332563-A.
 XX PD 07-DEC-1999.
 XX PF 26-MAY-1998; 98JP-0163034.
 XX PR 26-MAY-1998; 98JP-0163034.
 XX PR (ASAH) ASahi KASEI KOGYO KK.
 XX PA WPI; 2000-091351/08.
 XX DR N-PSDB; AAZ58664.
 XX PT An antibody and the nucleic acid coding the antibody -
 XX PS Disclosure; Page 17-18; 25pp; Japanese.

XX CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the L chain sequence of the antibody 4H5.
 XX SQ Sequence 305 AA;

Query Match 100.0%; Score 94; DB 21; Length 305;
 Best Local Similarity 100.0%; Pred. No. 9.4e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYNEMFKG 17
DB 72 EIYPGSGSAYNEMFKG 88
RESULT 10
ID AAY51141 standard; Protein; 305 AA.
XX AAY51141;
XX 31-MAR-2000 (first entry)
XX Murine derived protein fragment #3.
XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
XX hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
XX HIV infection; autoimmune disease; murine.
OS Mus sp.
XX WO9961629-A1.
XX 02-DEC-1999.
XX 24-MAY-1999; 99WO-JP02711.
XX 25-MAY-1998; 98JP-0159957.
XX 26-MAY-1998; 98JP-0163023.
XX (ASAH) ASAH KASEI KOGYO KK.
XX (ASAH) ASAH MEDICAL CO LTD.
XX Ono M, Soka T, Morimoto I, Miyamura K;
XX WPI; 2000-086720/07.
XX N-PSDB; AAZ44205.
XX Devices containing antibodies recognising CD4 or CD34 and their use for
XX the separation of CD4 or CD34 positive cells
XX Claim 22; Page 80-82; 111pp; Japanese.
XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for
XX the collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal
XX compositions for the treatment of HIV infection and autoimmune diseases.
XX This sequence represents a murine derived protein fragment which is used
XX to illustrate the method of the invention.
XX Sequence 305 AA;
Query Match 100.0%; Score 94; DB 21; Length 305;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIYPGSGSAYNEMFKG 17
DB 198 EIYPGSGSAYNEMFKG 214
RESULT 11
ID AAY51142 standard; Protein; 305 AA.
XX AAY51142;
XX 31-MAR-2000 (first entry)
XX Murine derived protein fragment #4.
XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
XX hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
XX HIV infection; autoimmune disease; murine.
OS Mus sp.
XX WO9961629-A1.
XX 02-DEC-1999.
XX 24-MAY-1999; 99WO-JP02711.
XX 25-MAY-1998; 98JP-0159957.
XX 26-MAY-1998; 98JP-0163023.
XX (ASAH) ASAH KASEI KOGYO KK.
XX (ASAH) ASAH MEDICAL CO LTD.
XX Ono M, Soka T, Morimoto I, Miyamura K;
XX WPI; 2000-086720/07.
XX N-PSDB; AAZ44205.
XX Devices containing antibodies recognising CD4 or CD34 and their use for
XX the separation of CD4 or CD34 positive cells
XX Claim 22; Page 82-84; 111pp; Japanese.
XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for
XX the collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal
XX compositions for the treatment of HIV infection and autoimmune diseases.
XX This sequence represents a murine derived protein fragment which is used
XX to illustrate the method of the invention.
XX Sequence 305 AA;
Query Match 100.0%; Score 94; DB 21; Length 305;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIYPGSGSAYNEMFKG 17
DB 198 EIYPGSGSAYNEMFKG 214
RESULT 11
ID AAY51142 standard; Protein; 305 AA.
XX AAY51142;
XX 31-MAR-2000 (first entry)

XX Murine derived protein fragment #4.
XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
XX hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
XX HIV infection; autoimmune disease; murine.
OS Mus sp.
XX WO9961629-A1.
XX 02-DEC-1999.
XX 24-MAY-1999; 99WO-JP02711.
XX 25-MAY-1998; 98JP-0159957.
XX 26-MAY-1998; 98JP-0163023.
XX (ASAH) ASAH KASEI KOGYO KK.
XX (ASAH) ASAH MEDICAL CO LTD.
XX Ono M, Soka T, Morimoto I, Miyamura K;
XX WPI; 2000-086720/07.
XX N-PSDB; AAZ44205.
XX Devices containing antibodies recognising CD4 or CD34 and their use for
XX the separation of CD4 or CD34 positive cells
XX Claim 22; Page 82-84; 111pp; Japanese.
XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for
XX the collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal
XX compositions for the treatment of HIV infection and autoimmune diseases.
XX This sequence represents a murine derived protein fragment which is used
XX to illustrate the method of the invention.
XX Sequence 305 AA;
Query Match 100.0%; Score 94; DB 21; Length 305;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIYPGSGSAYNEMFKG 17
DB 72 EIYPGSGSAYNEMFKG 88
RESULT 12
ID AAY51264 standard; peptide; 119 AA.
XX AAY51264;
XX 14-APR-2000 (first entry)
XX Monoclonal antibody MAK CD4 heavy chain variable region peptide.
XX Framework region; monoclonal antibody; variable domain; detection;
XX immunotherapy; MAK CD4.
XX Unidentified.
XX DE19828466-A1.
XX 30-DEC-1999.
XX 26-JUN-1998; 98DE-1028466.

PCT priority for instant

not a perfect match

XX 26-JUN-1998; 98DE-1028466.
 XX (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX Nussbaum S, Moessner E, Lenz H, Praast G;
 XX WPI; 2000-107255/10.
 XX Suppressor peptides derived from antibodies for use in immunoassays -
 XX Disclosure; Page 16; 20pp; German.
 XX This invention describes novel peptides derived from a framework region
 CC of the variable domain of an antibody for detection, immunotherapy or
 CC for scintigraphs. The peptides of the invention are used in a method to
 CC detect analytes in a sample by eliminating interference in the sample.
 CC AA51254-Y51267 represent peptides derived from the framework regions of
 CC the variable domain of an antibody which are used to illustrate the
 CC method of the invention.
 XX Sequence 119 AA;
 Query Match 93.6%; Score 88; DB 21; Length 119;
 Best Local Similarity 94.1%; Pred. No. 2.7e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EIYPGSGSAYYNEMFKG 17
 DB 50 EIYPGSGSAYYNEMFKG 66
 RESULT 13
 AAR32124
 ID AAR32124 standard; Protein; 137 AA.
 AC AAR32124;
 XX 02-JUN-1993 (first entry)
 XX Anti-CD4 antibody WT 3.10 heavy chain variable region.
 XX immunosuppression; tissue transplantation; graft; H chain; V region;
 KW T-helper cell inhibition; transplant rejection; MAB;
 KW interleukin-2 receptor.
 XX Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= signal
 FT Region 19..125
 FT /label= Variable
 FT Region 126..137
 FT /label= J3
 XX DE4143214-A.
 XX 28-JAN-1993.
 XX 30-DEC-1991; 91DE-4143214.
 XX 25-JUL-1991; 91DE-4124759.
 XX 30-DEC-1991; 91DE-4143214.
 XX (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX Kaluza B, Riethmueller G, Scheuer W, Weidle U;
 XX WPI; 1993-037582/05.
 XX N-PSDB; AAQ36610.
 XX Synergistic antibody compsn. for use as immunosuppressant -
 PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
 TT alpha- or anti-IL2R beta antibodies

XX Claim 5; Page 12; 18pp; German.
 XX This sequence is the heavy chain variable region of a preferred
 CC anti-CD4 monoclonal antibody for use in the claimed synergistic
 CC composition. MAB MT 3.10 is deposited as clone 3.101/SB10 (ECACC
 CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R
 CC alpha or beta antibody. Individually the antibodies are strongly
 CC inhibiting and when used together their immunosuppressive properties
 CC are improved; they synergistically inhibit T-helper cell
 CC proliferation to effectively inhibit transplant rejection at low
 CC doses without significantly reducing the general immune response.
 CC See also AAQ36608-Q36616.
 XX Sequence 137 AA;
 Query Match 93.6%; Score 88; DB 14; Length 137;
 Best Local Similarity 94.1%; Pred. No. 3.1e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EIYPGSGSAYYNEMFKG 17
 DB 68 EIYPGSGSAYYNEMFKG 84
 RESULT 14
 AAW07437
 ID AAW07437 standard; Protein; 121 AA.
 XX AC AAW07437;
 XX 12-AUG-1997 (first entry)
 XX Anti-DNA antibody 4b2 group heavy chain variable region.
 KW Heavy chain; variable region; anti-DNA; monoclonal; antibody;
 KW 4b2 group; hairpin; diagnosis; inflammatory glomerulonephritis;
 KW systemic lupus erythematosus; screening; treatment; prevention;
 KW SLE; disease; consensus; putative.
 XX OS Synthetic.
 XX Key Location/Qualifiers
 FT Region 1..30
 FT /label= framework_I
 FT Region 31..35
 FT /label= CDR_I
 FT Region 36..49
 FT /label= framework_II
 FT Region 50..66
 FT /label= CDR_II
 FT Region 67..98
 FT /label= framework_III
 FT Region 99..110
 FT /label= CDR_III
 FT Region 111..121
 FT /label= J_region
 XX WO9636361-A1.
 XX 21-NOV-1996.
 XX 16-MAY-1996; 96WO-US07113.
 XX 18-MAY-1995; 95US-0443540.
 XX (UNMI) UNIV MICHIGAN.
 XX Glick GD, Swanson PC;
 XX WPI; 1997-011854/01.
 XX N-PSDB; AAT43806.
 XX

PT Anti-DNA antibody which specifically binds DNA hairpin - useful to
 PT develop prods. for diagnosis and treatment of disorders, e.g.
 PT glomerulonephritis or systemic lupus erythematosus
 XX

PS Example; Fig 9; 102pp; English.

XX The present sequence is the heavy chain variable region of the
 CC group 4b2 putative consensus anti-DNA monoclonal antibody (Mab),
 CC which has a high affinity for single stranded DNA, low or no
 CC affinity for double stranded DNA and specifically binds a DNA
 CC hairpin. The Mab can be used to diagnose disorders associated with the
 CC pathological complexation of DNA, e.g. inflammatory
 CC glomerulonephritis and systemic lupus erythematosus. It can also be
 CC used to generate reagents to screen for pharmaceutical agents, and
 CC treat and/or prevent an above disorder.
 CC The sequence was derived by aligning homologous anti-DNA Mab,
 CC whose sequences have been published, as well as several Mab of
 CC other specificities obtained from a database search.

Sequence 121 AA;

Query Match 86.2%; Score 81; DB 18; Length 121;
 Best Local Similarity 82.4%; Pred. No. 0.00028;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYINEMFKG 17
 |||||: |||||
 Db 50 EIYPGSGNTYINEMFKG 66

RESULT 15

AAR79877
 ID AAR79877 standard; Protein; 123 AA.

XX AAR79877;

XX 24-MAY-1996 (first entry)

XX Anti-EGFR antibody heavy chain variable region (Clone L2 1C).

XX Single chain antibody; antibody; epidermal growth factor receptor;
 KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;
 KW assessment; phage antibody library.

XX Mus musculus.

Key	Location/Qualifiers
Region	1..30
FT	/label= Framework region 1.
FT	31..35
FT	/label= CDR1.
FT	36..49
FT	/label= Framework region 2.
FT	50..66
FT	/label= CDR2.
FT	67..98
FT	/label= Framework region 3.
FT	99..112
FT	/label= CDR3.
FT	113..123
FT	/label= Framework region 4.

XX WO9525167-A1.

XX 21-SEP-1995.

XX 16-MAR-1995; 95WO-EP00978.

XX 02-DEC-1994; 94EP-0118970.

XX 17-MAR-1994; 94EP-0104160.

XX (MERE) MERCK PATENT GMBH.

XX

PI Adan J, Ansell KH, Bendig MM, Blasco F, Guessow D;
 PI Kettleborough AC, Mitjans F, Piulats J, Rosell E;
 XX
 DR WPI; 1995-336972/43.
 XX

PT Anti-EGFR antibodies and single chain Fv antibody fragments -
 PT obtained from phage-antibody libraries, useful for diagnosis and
 PT therapy of tumours
 XX
 PS Disclosure; Figure 1A; 93pp; English.
 XX

CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies
 CC and antibodies constructed from anti-EGFR antibody fragments can be
 CC used for diagnosis of tumours and assessment of tumour growth in
 CC vitro and in vivo. They may also be used in a pharmaceutical
 CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.
 CC The antibodies and fragments are derived from mice but are humanised
 CC so as to cause minimum reaction against them. They are produced
 CC using the phage antibody library. (See AAT04011-T04026 and
 CC AAR79858-R79873)

XX Sequence 123 AA;

Query Match 80.9%; Score 76; DB 16; Length 123;
 Best Local Similarity 81.2%; Pred. No. 0.0015;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGSGSAYINEMFKG 17
 |||||: |||||
 Db 51 IYPGSGTYINEMFKG 66

Search completed: February 14, 2003, 11:15:42
 Job time : 47.0645 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	88	93.6	119	4	US-09-344-587-11	Sequence 11, Appl
2	81	86.2	98	3	US-08-881-037-64	Sequence 64, Appl
3	73	77.7	113	3	US-08-881-037-18	Sequence 18, Appl
4	73	77.7	121	3	US-08-881-037-65	Sequence 65, Appl
5	71	75.5	355	3	US-08-875-811-57	Sequence 57, Appl
6	68	72.3	91	2	US-08-713-939A-70	Sequence 70, Appl
7	68	72.3	91	2	US-08-713-939A-78	Sequence 78, Appl
8	68	72.3	91	4	US-09-036-579-70	Sequence 70, Appl
9	68	72.3	91	4	US-09-036-579-78	Sequence 78, Appl
10	68	72.3	91	4	US-09-550-374-70	Sequence 70, Appl
11	68	72.3	91	4	US-09-550-374-78	Sequence 78, Appl
12	68	72.3	92	2	US-08-713-939A-79	Sequence 79, Appl
13	68	72.3	92	2	US-08-713-939A-85	Sequence 85, Appl
14	68	72.3	92	4	US-09-036-579-79	Sequence 79, Appl
15	68	72.3	92	4	US-09-036-579-85	Sequence 85, Appl
16	68	72.3	92	4	US-09-550-374-79	Sequence 79, Appl
17	68	72.3	92	4	US-09-550-374-85	Sequence 85, Appl
18	68	72.3	95	2	US-08-713-939A-86	Sequence 86, Appl
19	68	72.3	95	4	US-09-036-579-86	Sequence 86, Appl
20	68	72.3	95	4	US-09-550-374-86	Sequence 86, Appl
21	68	72.3	101	2	US-08-713-939A-82	Sequence 82, Appl
22	68	72.3	101	4	US-09-036-579-82	Sequence 82, Appl
23	68	72.3	101	4	US-09-550-374-82	Sequence 82, Appl
24	68	72.3	103	2	US-08-713-939A-84	Sequence 84, Appl
25	68	72.3	103	4	US-09-036-579-84	Sequence 84, Appl
26	68	72.3	103	4	US-09-550-374-84	Sequence 84, Appl
27	68	72.3	108	2	US-08-713-939A-83	Sequence 83, Appl

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kanski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX:
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-037-64

Query Match 86.2%; Score 81; DB 3; Length 98;
Best Local Similarity 82.4%; Pred. No. 6e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 EIIYPGSGSAYYNEMFKG 17
|||||: |||||
DB 50 EIIYPSGNTYNEKFKG 66

RESULT 3
US-08-881-037-18
Sequence 18, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Klick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kanski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792

TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-037-18

Query Match 77.7%; Score 73; DB 3; Length 113;
Best Local Similarity 76.5%; Pred. No. 0.00099;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIIYPGSGSAYYNEMFKG 17
|||||: |||||
DB 42 EIIYPSGNTYNEKFKG 58

RESULT 4
US-08-881-037-65
Sequence 65, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Klick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kanski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX:

INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-037-65

Query Match 77.7%; Score 73; DB 3; Length 121;
Best Local Similarity 76.5%; Pred. No. 0.0011;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIIYPGSGSAYYNEMFKG 17
|||||: |||||
DB 50 EIIYPSGNTYNEKFKG 66

RESULT 5

us-09-701-001b-2.ra1

Fri Feb 14 15:00:50 2003

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US-08-875-811-57
; Sequence 57, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Luis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-57
Query Match 75.5%; Score 71; DB 3; Length 355;
Best Local Similarity 70.6%; Pred. No. 0.0062;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17
Db 168 DIYPGSDNTYNEKFKG 184

RESULT 6
US-08-713-939A-70
; Sequence 70, Application US/08713939A
; Patent No. 5846533
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,939A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
;

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,939A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX:
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-713-939A-70
Query Match 72.3%; Score 68; DB 2; Length 91;
Best Local Similarity 70.6%; Pred. No. 0.0042;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17
Db 24 EIWPRSGNTYNEKFKG 40

RESULT 7
US-08-713-939A-78
; Sequence 78, Application US/08713939A
; Patent No. 5846533
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,939A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
;

```

TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-713-939A-78

Query Match 72.3%; Score 68; DB 2; Length 91;
Best Local Similarity 70.6%; Pred. No. 0.0042;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIYPGSGSAYNNEMFKG 17
Db 24 EIWPRSGNTYYNEKFG 40

RESULT 8

US-09-036-579-70
Sequence 70, Application US/09036579
Patent No. 6290954

GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,579
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,939
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:

INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-036-579-70

Query Match 72.3%; Score 68; DB 4; Length 91;
Best Local Similarity 70.6%; Pred. No. 0.0042;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIYPGSGSAYNNEMFKG 17
Db 24 EIWPRSGNTYYNEKFG 40

RESULT 9

US-09-036-579-78
Sequence 78, Application US/09036579
Patent No. 6290954

GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,579
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,939
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:

INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-036-579-78

Query Match 72.3%; Score 68; DB 4; Length 91;
Best Local Similarity 70.6%; Pred. No. 0.0042;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIYPGSGSAYNNEMFKG 17
Db 24 EIWPRSGNTYYNEKFG 40

RESULT 10

US-09-550-374-70
Sequence 70, Application US/09550374
Patent No. 6372214

GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,579
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,939
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:

INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-550-374-70

Query Match 72.3%; Score 68; DB 4; Length 91;
Best Local Similarity 70.6%; Pred. No. 0.0042;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIYPGSGSAYNNEMFKG 17
Db 24 EIWPRSGNTYYNEKFG 40

Fri Feb 14 15:00:50 2003

ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/550,374
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/036,579
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-550-374-70

Query Match 72.3%; Score 68; DB 4; Length 91;
Best Local Similarity 70.6%; Pred. No. 0.0042;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVPGSGSAYYNEMFKG 17
||| ||: |||| ||||
Db 24 EIWPRSGNTYYNEKFKG 40

RESULT 11
US-09-550-374-78
; Sequence 78, Application US/09550374
; Patent No. 6372214
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/550,374
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/036,579
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-550-374-78

Query Match 72.3%; Score 68; DB 4; Length 91;
Best Local Similarity 70.6%; Pred. No. 0.0042;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVPGSGSAYYNEMFKG 17
||| ||: |||| ||||
Db 24 EIWPRSGNTYYNEKFKG 40

RESULT 12
US-08-713-939A-79
; Sequence 79, Application US/08713939A
; Patent No. 5846533
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,939A
FILING DATE: 13-SEP-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-713-939A-79

Query Match 72.3%; Score 68; DB 2; Length 92;
Best Local Similarity 70.6%; Pred. No. 0.0043;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVPGSGSAYYNEMFKG 17
||| ||: |||| ||||

Db 25 EIWRSGNTYYNEKPKG 41

RESULT 13

US-08-713-939A-85
; Sequence 85, Application US/08713939A
; Patent No. 5845533
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,939A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX:
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-713-939A-85

Query Match 72.3%; Score 68; DB 2; Length 92;
Best Local Similarity 70.6%; Pred. No. 0.0043;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEKPKG 17
||:| ||: |||| |||
Db 25 EIWRSGNTYYNEKPKG 41

RESULT 14

US-09-036-579-79
; Sequence 79, Application US/09036579
; Patent No. 6290954
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA

; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,579
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,939
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX:
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-036-579-79

Query Match 72.3%; Score 68; DB 4; Length 92;
Best Local Similarity 70.6%; Pred. No. 0.0043;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEKPKG 17
||:| ||: |||| |||
Db 25 EIWRSGNTYYNEKPKG 41

RESULT 15

US-09-036-579-85
; Sequence 85, Application US/09036579
; Patent No. 6290954
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,579
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,939
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001

us-09-701-001b-2.ra

Fri Feb 14 15:00:50 2003

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-854-5277
 TELEFAX: 415-854-0875
 TELEX:
 INFORMATION FOR SEQ ID NO: 85:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 92 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-036-579-85

Query Match 72.3%; Score 68; DB 4; Length 92;
 Best Local Similarity 70.6%; Pred. No. 0.0043;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 EIYPGSGSAYNYEMFKG 17
 ||| ||: |||| |||
 25 EIWPRSGNTYYNFKG 41

Search completed: February 14, 2003, 11:20:47
 Job time : 15.3548 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:15:53 ; Search time 9,87097 Seconds
(without alignments)
44.001 Million cell updates/sec

Title: US-09-701-001b-2

Perfect score: 94

Sequence: 1 E1YPGSGSAYNEMFKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Matched: 140259 seqs, 25548876 residues -

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
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- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	72.3	91	10	US-09-943-906-70
2	68	72.3	91	10	US-09-943-906-78
3	68	72.3	92	10	US-09-943-906-79
4	68	72.3	92	10	US-09-943-906-85
5	68	72.3	95	10	US-09-943-906-86
6	68	72.3	101	10	US-09-943-906-82
7	68	72.3	103	10	US-09-943-906-84
8	68	72.3	108	10	US-09-943-906-83
9	68	72.3	114	10	US-09-943-906-68
10	68	72.3	114	10	US-09-943-906-76
11	68	72.3	114	10	US-09-943-906-77
12	66	70.2	117	9	US-09-144-886-71
13	66	70.2	138	1	US-08-779-784-31
14	65	69.1	17	10	US-09-861-294-15
15	65	69.1	153	10	US-09-861-294-4
16	64	68.1	105	10	US-09-943-906-75
17	64	68.1	114	10	US-09-943-906-69
18	62	66.0	31	9	US-09-956-206A-31
19	62	66.0	91	10	US-09-943-906-71

20	62	66.0	91	10	US-09-943-906-81	Sequence 81, Appl
21	62	66.0	99	10	US-09-943-906-80	Sequence 80, Appl
22	62	66.0	119	10	US-09-839-447A-1	Sequence 1, Appl
23	62	66.0	139	12	US-10-006-773-13	Sequence 13, Appl
24	60	63.8	140	9	US-09-905-928-6	Sequence 6, Appl
25	59	62.8	117	9	US-09-144-886-72	Sequence 72, Appl
26	59	62.8	515	10	US-09-825-012-66	Sequence 66, Appl
27	59	62.8	517	10	US-09-825-012-38	Sequence 38, Appl
28	59	62.8	519	10	US-09-825-012-76	Sequence 76, Appl
29	59	62.8	519	10	US-09-825-012-80	Sequence 80, Appl
30	59	62.8	521	10	US-09-825-012-71	Sequence 71, Appl
31	59	62.8	525	10	US-09-825-012-85	Sequence 85, Appl
32	59	62.8	527	10	US-09-825-012-43	Sequence 43, Appl
33	59	62.8	529	10	US-09-825-012-95	Sequence 95, Appl
34	59	62.8	531	10	US-09-825-012-90	Sequence 90, Appl
35	59	62.8	729	10	US-09-825-012-52	Sequence 52, Appl
36	59	62.8	730	10	US-09-825-012-49	Sequence 49, Appl
37	59	62.8	731	10	US-09-825-012-46	Sequence 46, Appl
38	59	62.8	739	10	US-09-825-012-61	Sequence 61, Appl
39	59	62.8	740	10	US-09-825-012-58	Sequence 58, Appl
40	59	62.8	741	10	US-09-825-012-55	Sequence 55, Appl
41	58	61.7	20	10	US-09-839-447A-9	Sequence 9, Appl
42	57	60.6	17	9	US-10-146-305-13	Sequence 13, Appl
43	57	60.6	138	9	US-10-146-305-8	Sequence 8, Appl
44	56	59.6	118	9	US-10-141-908-2	Sequence 2, Appl
45	56	59.6	118	9	US-10-141-908-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-943-906-70

Sequence 70, Application US/09943906

Patent No. US20020150571A1

GENERAL INFORMATION:

APPLICANT: Prusiner, Stanley B.

Williamson, R. Anthony

Burton, Dennis R.

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 2200 Sand Hill Road

CITY: Menlo Park

STATE: CA

COUNTRY: U.S.A.

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/943,906

FILING DATE: 30-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/550,374

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Bozicevic, Karl

REGISTRATION NUMBER: 28,807

REFERENCE/DOCKET NUMBER: 06510/059001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-854-5277

TELEFAX: 415-854-0875

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 91 amino acids

TYPE: amino acid

STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-09-943-906-70

Query Match      72.3%; Score 68; DB 10; Length 91;
Best Local Similarity 70.6%; Pred. No. 0.0021;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIYPGSGSAYYNEKFKG 17
   |||||
Db 24 EIWPRSGNTYYNEKFKG 40

RESULT 2
US-09-943-906-78
; Sequence 78, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
;              Williamson, R. Anthony
;              Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-09-943-906-78

Query Match      72.3%; Score 68; DB 10; Length 91;
Best Local Similarity 70.6%; Pred. No. 0.0021;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIYPGSGSAYYNEKFKG 17
   |||||
Db 24 EIWPRSGNTYYNEKFKG 40

RESULT 3
US-09-943-906-79
; Sequence 79, Application US/09943906
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
;              Williamson, R. Anthony
;              Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-943-906-79

Query Match      72.3%; Score 68; DB 10; Length 92;
Best Local Similarity 70.6%; Pred. No. 0.0021;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIYPGSGSAYYNEKFKG 17
   |||||
Db 25 EIWPRSGNTYYNEKFKG 41

RESULT 4
US-09-943-906-85
; Sequence 85, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
;              Williamson, R. Anthony
;              Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-943-906-86
Query Match 72.3%; Score 68; DB 10; Length 95;
Best Local Similarity 70.6%; Pred. No. 0.0022;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EYPGSGSAYNEMFKG 17
||:| ||: |||| |||
Db 28 EIWPRSGNTYNEKFKG 44

RESULT 6
US-09-943-906-82
; Sequence 82, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamson, R. Anthony
; Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 82:
US-09-943-906-82
Query Match 72.3%; Score 68; DB 10; Length 101;
Best Local Similarity 70.6%; Pred. No. 0.0023;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EYPGSGSAYNEMFKG 17
Db 34 EIWPRSGNTYNEKFKG 50

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; COUNTRY: U.S.A.
; ZIP: 94025
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ version 2.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
;
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 83:
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; US-09-943-906-83
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; Query Match 72.3% Score 68; DB 10; Length 108;
; Best Local Similarity 70.6% Pred. No. 0.0025;
; Matches 12; Conservative 2; Mismatches 3; Indels
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; QY 1 EYPGSGSAYINEMFKG 17
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; Ddb 41 EIWPRSGTYNEKFG 57
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; RESULT 9
;
; US-09-943-906-68
; Sequence 68, Application US/09943906
; Patent No. US20020150571al
;
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamsson, R. Anthony
; Burton, Dennis R.
;
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807

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Query Match 72.3%; Score 68; DB 10; Length 114;
Best Local Similarity 70.6%; Pred. No. 0.0026;

FILE OF INVENTION: Botulinum
TITLE OF INVENTION: Botulinum
FILE REFERENCE: 2500.117USO

0:

; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: IG5 region VH epitope 3
US-09-144-886-71

Query Match 70.2%; Score 66; DB 9; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.0052;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYVNEFK 16
Db 50 DIYPGSGSTNYNEFK 65

RESULT 13
US-08-779-784-31
; Sequence 31, Application US/08779784
; Patent No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:

; ORGANISM: Mus musculus
US-08-779-784-31

Query Match 70.2%; Score 66; DB 1; Length 138;
Best Local Similarity 75.0%; Pred. No. 0.0061;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGSGSAYVNEFK 17
Db 70 IYPGSGSTKYNEFK 85

RESULT 14
US-09-861-294-15
; Sequence 15, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-861-294-15

Query Match 69.1%; Score 65; DB 10; Length 17;
Best Local Similarity 62.5%; Pred. No. 0.0011;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGSAYVNEFK 17
Db 2 IYPGSGDTYINOKFK 17

RESULT 15
US-09-861-294-4
; Sequence 4, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-09-861-294-4

Query Match 69.1%; Score 65; DB 10; Length 153;

us-09-701-001b-2.rapb

Fri Feb 14 15:00:51 2003

Best Local Similarity 62.5%; Pred. No. 0.0094; 3; Mismatches 3; Indels 0; Gaps 0;

Matches 10; Conservative

Qy 2 IYPGSGSAYYNEMFKG 17

|:|:| | | | |

Db 70 IFFGNGDTYYNQKFKG 85

Search completed: February 14, 2003, 11:21:29

Job time : 9.87097 secs

Fri Feb 14 15:00:51 2003

GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: February 14, 2003, 11:12:02 ; Search time 17 seconds
(without alignments)
96.134 Million cell updates/sec

Title: US-09-701-001B-2
Perfect score: 94
Sequence: 1 E1YPGSGSAYNEMFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Sched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	88	93.6	119	2 S19964	Ig heavy chain v r
2	88	93.6	137	2 PH1227	Ig heavy chain pre
3	82	87.2	117	2 S19966	Ig heavy chain v r
4	81	86.2	110	2 PH1000	Ig heavy chain v r
5	78	83.0	475	2 S01321	Ig gamma-2b chain
6	76	80.9	96	2 PH1165	Ig heavy chain v r
7	73	77.7	94	2 G32513	Ig heavy chain v r
8	72	76.6	95	2 G37262	Ig heavy chain v r
9	72	76.6	111	2 PH0988	Ig heavy chain v r
10	71	75.5	119	2 E30562	Ig heavy chain v r
11	69	73.4	121	2 S19969	Ig heavy chain v r
12	67	71.3	67	2 H28833	Ig kappa chain v r
13	67	71.3	107	2 PH0999	Ig heavy chain v r
14	67	71.3	109	2 PH0997	Ig heavy chain v r
15	67	71.3	111	2 PH0998	Ig heavy chain v r
16	67	71.3	119	2 C30562	Ig heavy chain v r
17	67	71.3	119	2 C30562	Ig heavy chain v r
18	67	71.3	246	2 S38950	Ig gamma chain - m
19	67	71.3	446	2 S40295	Ig gamma-2a chain
20	66	70.2	104	2 S26466	Ig heavy chain v r
21	66	70.2	117	1 HVMSA1	Ig heavy chain pre
22	66	70.2	137	2 S09956	Ig heavy chain v r
23	65	69.1	120	2 PD0008	Ig heavy chain v r
24	65	69.1	120	2 PD0008	Ig heavy chain v r
25	64	68.1	90	2 PH1159	Ig heavy chain v r
26	64	68.1	94	2 S42185	Ig gamma chain v r
27	64	68.1	106	2 PH1002	Ig heavy chain v r
28	64	68.1	109	2 PH1001	Ig heavy chain v r
29	64	68.1	115	2 A54378	Ig heavy chain v r

30	64	68.1	117	2 S03289	Ig heavy chain pre
31	62	66.0	76	2 B28572	Ig heavy chain v r
32	62	66.0	116	2 B28814	Ig heavy chain v r
33	61	64.9	115	2 A56700	Ig heavy chain (an
34	61	64.9	122	2 S06825	Ig heavy chain v r
35	61	64.9	214	2 PC4202	monoclonal antibod
36	60	63.8	93	2 S42182	Ig gamma chain v r
37	60	63.8	94	2 S42177	Ig gamma chain v r
38	60	63.8	95	2 S42178	Ig gamma chain v r
39	60	63.8	97	2 S42181	Ig gamma chain v r
40	60	63.8	101	2 S42179	Ig gamma chain v r
41	60	63.8	101	2 S42184	Ig gamma chain v r
42	60	63.8	102	2 S42180	Ig gamma chain v r
43	60	63.8	137	2 E29380	Ig heavy chain pre
44	60	63.8	469	2 S37483	Ig gamma-2a chain
45	59	62.8	116	2 S26309	Ig heavy chain v r

ALIGNMENTS

RESULT 1

S19964
Ig heavy chain v region (M-T310) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999
C:Accession: S19964
R:Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19964
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <WEI>
A:Cross-references: EMBL:X65084; NID:g51964; PIDN:CAA46212.1; PID:g51965
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.6%; Score 88; DB 2; Length 119;
Best Local Similarity 94.1%; Pred. No. 9.3e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 E1YPGSGSAYNEMFKG 17
Db 50 E1YPGSGSAYNEMFKG 66

RESULT 2

PH1227
Ig heavy chain precursor v region (M-T310) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 23-Jul-1999
C:Accession: PH1227
R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Fliieger, D.; L; Gene 121, 271-278, 1992
A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and A:Reference number: PH1224; MUID:93077041; PMID:1446824
A:Accession: PH1227
A:Molecule type: mRNA
A:Residues: 1-137 <WEI>
A:Cross-references: GB:S50266; NID:g260767; PIDN:AAB24321.1; PID:g260768
C:Note: this mouse sequence was hybridized and fused with a human constant region gen C:Superfamily: Immunoglobulin V region; immunoglobulin homology
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-137/Product: Ig heavy chain V region #status predicted <WAT>
F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 93.6%; Score 88; DB 2; Length 137;
Best Local Similarity 94.1%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17
 Db 68 EIYPGSGSAYYNEMFKG 84

RESULT 3

Ig heavy chain V region (M-T404) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 16-Aug-1996
 C:Accession: S19966
 R:Weissenhorn, W.; Rietmueller, G.; Weiss, E.M.; Rieber, E.P.
 Submitted to the EMBL Data Library, March 1992
 A:Description: Structural characterization of CD4 mAb.
 A:Reference number: S19963
 A:Accession: S19966
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-117 <WEI>

A:Cross-references: EMBL:X65085
 Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 82; DB 2; Length 117;
 Best Local Similarity 88.2%; Pred. No. 8.1e-06;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17
 Db 50 EIYPGSGSAYYNEMFKG 66

RESULT 4

Ig heavy chain V region (clone 202.105) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1000
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH1000
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-110 <TIL>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 81; DB 2; Length 110;
 Best Local Similarity 82.4%; Pred. No. 1.1e-05;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17
 Db 50 EIYPGSGSAYYNEMFKG 66

RESULT 5

Ig gamma-2b chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
 C:Accession: S01321
 R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
 Eur. J. Biochem. 176, 287-295, 1988
 A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
 A:Reference number: S01320; MUID:88329081; PMID:3138116
 A:Accession: S01321

A:Molecule type: mRNA
 A:Residues: 1-475 <DEI>
 A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
 A:Note: this sequence was determined from the differentiated gene
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
 F:159-223/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 78; DB 2; Length 475;
 Best Local Similarity 76.5%; Pred. No. 0.00016;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17
 Db 69 EIYPGSGSAYYNEMFKG 85

RESULT 6

Ig heavy chain V region (clone 26F.1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PH1165
 R:Schitteck, B.; Rajewsky, K.
 J. Exp. Med. 176, 427-438, 1992
 A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
 A:Reference number: PH1105; MUID:92364545; PMID:1500855
 A:Accession: PH1165
 A:Molecule type: DNA
 A:Residues: 1-96 <SCH>

A:Experimental source: B cell
 Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-96/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 76; DB 2; Length 96;
 Best Local Similarity 81.2%; Pred. No. 5.9e-05;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEMFKG 17
 Db 51 IYPGSGNTYNNEMFKG 66

RESULT 7

Ig heavy chain V region (BXW14) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 16-Aug-1996
 C:Accession: G32513
 R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.
 J. Clin. Invest. 82, 852-860, 1988
 A:Title: Immunoglobulin kappa light chain variable region gene complex organization a
 A:Reference number: A94689; MUID:88331394; PMID:3138286
 A:Accession: G32513
 A:Molecule type: DNA
 A:Residues: 1-94 <KOF>

Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 77.7%; Score 73; DB 2; Length 94;
 Best Local Similarity 76.5%; Pred. No. 0.00017;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17
 Db 25 EIYPGSGNTYNNEMFKG 41

RESULT 8

G37262

Ig heavy chain V region (14D2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 16-Aug-1996
C:Accession: G37262
R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: G37262
A:Molecule type: mRNA
A:Status: preliminary; not compared with conceptual translation
A:Residues: 1-95 <GOS>
A:Cross-references: GB:M57993
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-84/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 72; DB 2; Length 95;
Best Local Similarity 76.5%; Pred. No. 0.00025;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17
Db 36 ETLPGSGSSYYNEKFKG 52
||||| ||| |||

RESULT 9
PH0988
Ig heavy chain V region (clone 17s-c3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH0988
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH0988
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-111 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 72; DB 2; Length 111;
Best Local Similarity 76.5%; Pred. No. 0.0003;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17
Db 50 EIYPRSGNIYYNEKFKG 66
||||| ||| ||| |||

RESULT 10
E30562
Ig heavy chain V region (27.10.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C:Accession: E30562
R:Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.I.
J. Immunol. 142, 888-893, 1989
A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site
A:Reference number: A30562; MUID:89110066; PMID:2464031
A:Accession: E30562
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SIK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 71; DB 2; Length 119;

Best Local Similarity 76.5%; Pred. No. 0.00046;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17
Db 50 EIYPGSGSTKYNEKFKG 66
||||| ||| |||

RESULT 11
S19969
Ig heavy chain V region (M-T413) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999
C:Accession: S19969
R>Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
Submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19969
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-121 <WEI>
A:Cross-references: EMBL:X65086; NID:951974; PIDN:CAA46214.1; PID:951975
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.4%; Score 69; DB 2; Length 121;
Best Local Similarity 81.2%; Pred. No. 0.00098;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFK 16
Db 50 EIYPGSGSNYYNENLK 65
||||| ||| |||

RESULT 12
H28833
Ig kappa chain V region (HP22.202.16) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-May-1997
C:Accession: H28833
R:Corbet, S.; Hirn, M.; Roth, C.; Theze, J.; Fougereau, M.; Schiff, C.
J. Immunol. 141, 779-784, 1988
A:Title: Allelic manipulation of the CAT idiotype cascade. Immunization of C57BL/6 mice with a monoclonal anti-idiotypic cascade.
A:Reference number: A92827; MUID:88285674; PMID:3135311
A:Accession: H28833
A:Molecule type: mRNA
A:Residues: 1-67 <COR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 71.3%; Score 67; DB 2; Length 67;
Best Local Similarity 75.0%; Pred. No. 0.0011;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEMFKG 17
Db 20 IYPGSGNTKYNEKFKG 35
||||| ||| |||

RESULT 13
PH0999
Ig heavy chain V region (clone 74-cl) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH0999
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH0999
A:Status: nucleic acid sequence not shown

Job time : 17 secs

A:Molecule type: mRNA
A:Residues: 1-107 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 67; DB 2; Length 107;
Best Local Similarity 75.0%; Pred. No. 0.0018;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEMFKG 17
|||||: ||| |||
Db 50 IYPGSGNTRYNEKFKG 65

RESULT 14

PH0997
Ig heavy chain V region (clone 17s-c2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
Accession: PH0997
J. Hillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
A:Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH0997
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-109 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 67; DB 2; Length 109;
Best Local Similarity 75.0%; Pred. No. 0.0018;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEMFKG 17
|||||: ||| |||
Db 51 IYPGSGNTRYNEKFKG 66

RESULT 15

PH0998
Ig heavy chain V region (clone 165.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
Accession: PH0998
J. Hillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
A:Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH0998
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-111 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 67; DB 2; Length 111;
Best Local Similarity 75.0%; Pred. No. 0.0018;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEMFKG 17
|||||: ||| |||
Db 51 IYPGSGNTRYNEKFKG 66

Search completed: February 14, 2003, 11:19:44

Fri Feb 14 15:00:51 2003

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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:05:27 ; Search time 8.77419 Seconds
(without alignments)
80.360 Million cell updates/sec

Title: US-09-701-001B-2
Perfect score: 94
Sequence: 1 EIYPGSGSAYNEMFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues 112892
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	70.2	117	1 HV52_MOUSE	P06327 mus musculus
2	52	55.3	120	1 HV03_MOUSE	P01747 mus musculus
3	52	55.3	121	1 HV01_MOUSE	P01745 mus musculus
4	51	54.3	140	1 HV02_MOUSE	P01746 mus musculus
5	48	51.1	117	1 HV04_MOUSE	P01748 mus musculus
6	48	51.1	372	1 Y983_CAME	P45492 campylobact
7	47	50.0	117	1 HV12_MOUSE	P01756 mus musculus
8	47	50.0	117	1 HV13_MOUSE	P01757 mus musculus
9	47	50.0	118	1 HV51_MOUSE	P06330 mus musculus
10	46	48.9	608	1 ATOS_ECOLI	Q06067 escherichia
11	45	47.9	138	1 HV48_MOUSE	P03980 mus musculus
12	45	47.9	117	1 HV05_MOUSE	P01749 mus musculus
13	45	47.9	576	1 PEX5_PICPA	P33292 picchia past
14	45	47.9	1353	1 VGL2_CVHOC	P36334 human coron
15	45	47.9	1363	1 VGL2_CVBF	P25190 bovine coro
16	45	47.9	1363	1 VGL2_CVBL9	P25191 bovine coro
17	45	47.9	1363	1 VGL2_CVBL	P25192 bovine coro
18	45	47.9	1363	1 VGL2_CVBL	P15777 bovine coro
19	45	47.9	1363	1 VGL2_CVBO	P25193 bovine coro
20	45	47.9	1363	1 VGL2_CVBO	P25194 bovine coro
21	44	46.8	117	1 HV09_MOUSE	P01753 mus musculus
22	44	46.8	117	1 HV10_MOUSE	P01754 mus musculus
23	44	46.8	117	1 HV14_MOUSE	P01758 mus musculus
24	44	46.8	117	1 HV07_MOUSE	P06328 mus musculus
25	44	46.8	139	1 HV07_MOUSE	P01751 mus musculus
26	44	46.8	405	1 SDC3_CHICK	P26261 gallus gall
27	43	45.7	212	1 RPY1_YEAST	P35718 saccharomyc
28	42	44.7	117	1 HV06_MOUSE	P01750 mus musculus
29	42	44.7	120	1 HV50_MOUSE	Q06329 mus musculus
30	42	44.7	442	1 SDC3_MOUSE	Q64519 mus musculus
31	42	44.7	442	1 SDC3_RAT	P33671 rattus norv
32	42	44.7	503	1 CPV2_PIG	P79430 sus scrofa
33	42	44.7	879	1 GUN1_CLOTH	Q02934 clostridium

34	42	44.7	986	1 GUNZ_CLOSR	P23659 clostridium
35	41	43.6	163	1 SPAS_ECOLI	P13430 escherichia
36	41	43.6	469	1 YXIA_BACSU	P42293 bacillus su
37	41	43.6	683	1 AMOH_ARTGO	Q59118 arthrobacte
38	41	43.6	695	1 MDLI_YEAST	P33310 saccharomyc
39	41	43.6	976	1 KIT_HUMAN	P10721 homo sapien
40	40	42.6	101	1 RM06_MARPO	P26861 marchantia
41	40	42.6	117	1 HV55_MOUSE	P18526 mus musculu
42	40	42.6	137	1 HV11_MOUSE	P01755 mus musculu
43	40	42.6	257	1 DLHH_SULSO	P95862 sulfolobus
44	40	42.6	489	1 OCLN_POTIR	Q28793 potorous tr
45	40	42.6	502	1 SPEL_LYCES	P49726 lycopersico

ALIGNMENTS

RESULT 1
HV52_MOUSE STANDARD; PRT: 117 AA.
AC P06327:
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH58 Al/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=85099340; PubMed=2578321;
RX Yancopoulos G.D., Alt F.W.;
RA "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
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CC -----
DR EMBL; M13787; AAA38499.1;
DR PIR; A02029; HVMSA1.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;
IG HEAVY CHAIN V REGION VH58 Al/A4.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.

Query Match 70.2%; Score 66; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.0006; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 4;
Qy 2 IYPGSGSAYNEMFKG 17
Db 70 IYPGSGSKYNEFKG 85

```
RESULT 2
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idio-type response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
DR PIR: A02028; HVMSG7.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 55.3%; Score 52; DB 1; Length 120;
Best Local Similarity 62.5%; Pred. No. 0.12;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEFKG 17
| ||:| ||| |||
DB 50 INPGNGYTKYNEFKG 65

RESULT 3
HV01_MOUSE
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3391-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RA Nucleic Acids Res. 8:4839-4840(1980).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR: A02027; GYMS11.
DR HSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.

RESULT 4
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 93g7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
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CC -----
CC EMBL; J00493; AAA38128.1; -.
CC PIR: A02028; HVMSG7.
CC HSP: P01810; 2FBJ.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam: PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 54.3%; Score 51; DB 1; Length 140;
Best Local Similarity 62.5%; Pred. No. 0.21;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEFKG 17
| ||:| ||| |||
DB 70 INPGNGYTKYNEFKG 85

RESULT 5
HV04_MOUSE
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
```

DE Ig heavy chain V region 23 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.; variable region contribution to the NPB family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.;
 RL Cell 24:625-637(1981).
 CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 DR PIR: A02030; HVMS23.
 DR HSSP: P01810; 2FBJ.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; Igv; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;
 Query Match 51.1%; Score 48; DB 1; Length 117;
 Best Local Similarity 60.0%; Pred. No. 0.54;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 2 IYPGSGSAYNEMFK 16
 DB 70 INPGNGGTNYNEKFK 84
 RESULT 6
 Y983_CAMJE STANDARD; PRT; 372 AA.
 ID P45492; Q9PNV6;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical lipoprotein Cj0983 precursor.
 GN Cj0983.
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
 OC Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 43431 / TGH 9011;
 RX MEDLINE=95247673; PubMed=7730270;
 RA Hani E.K., Chan V.L.;
 RA "Expression and characterization of Campylobacter jejuni
 RT benzoylglutamate amidohydrolase (Hippuricase) gene in Escherichia
 RT coli".
 RL J. Bacteriol. 177:2396-2402(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCTC 11168;
 RX MEDLINE=20150912; PubMed=10688204;
 RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churche C.,
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
 RA Jags J.K., Karyshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

RA Whitehead S., Barrell B.G.;
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
 RT reveals hypervariable sequences.";
 RL Nature 403:665-668(2000).
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 CC (Potential).
 CC [1]
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 CC [2]
 CC EMBL: Z36940; CAA85399.1;
 CC EMBL: ALI39076; CAB73239.1;
 KW Hypothetical protein; Membrane; Lipoprotein; Signal;
 KW Complete proteome.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 372 HYPOTHETICAL LIPOPROTEIN Cj0983.
 FT LIPID 18 18 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT CONFLICT 78 78 T -> A (IN REF. 1).
 FT CONFLICT 83 83 D -> N (IN REF. 1).
 FT CONFLICT 105 105 K -> E (IN REF. 1).
 FT CONFLICT 157 157 S -> R (IN REF. 1).
 FT CONFLICT 227 227 V -> A (IN REF. 1).
 FT CONFLICT 230 230 K -> E (IN REF. 1).
 FT CONFLICT 278 278 A -> T (IN REF. 1).
 FT CONFLICT 289 289 A -> T (IN REF. 1).
 FT CONFLICT 353 353 A -> V (IN REF. 1).
 FT CONFLICT 370 371 AS -> SYFK (IN REF. 1).
 SQ SEQUENCE 372 AA; 42164 MW; 3C562051EBC638B4 CRC64;
 Query Match 51.1%; Score 48; DB 1; Length 372;
 Best Local Similarity 45.5%; Pred. No. 1.9;
 Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 1;
 QY 1 EYPGSGSA-----YNNEMFK 16
 DB 100 EYKGNKASISIKREYNDLFK 121
 RESULT 7
 HV12_MOUSE STANDARD; PRT; 117 AA.
 ID P01756;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ig heavy chain V region MOPC 104E.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
 RX MEDLINE=83075344; PubMed=6816276;
 RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
 RA Hood L.E.;
 RA "Complete amino acid sequence of a mouse mu chain: homology among
 RT heavy chain constant region domains";
 RL Biochemistry 21:5415-5424(1982).
 CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
 CC PROTEIN HAS ALSO BEEN DETERMINED.
 CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 CC PIR: A02039; MHMS4E.
 DR HSSP: P01789; IMCP.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; Igv; 1.
 KW Immunoglobulin V region; Glycoprotein.

```

FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 50.0%; Score 47; DB 1; Length 117;
Best Local Similarity 47.1%; Pred. No. 0.78;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17
:| | | | | | | | | |
DB 50 DINPNNGGTSYNQKFKG 66

RESULT 8
HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MIMJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 50.0%; Score 47; DB 1; Length 117;
Best Local Similarity 47.1%; Pred. No. 0.78;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17
:| | | | | | | | | |
DB 50 DINPNNGGTSYNQKFKG 66

RESULT 9
HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Diidrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

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RT "A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBL J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 50.0%; Score 47; DB 1; Length 118;
Best Local Similarity 47.1%; Pred. No. 0.79;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17
:| | | | | | | | | |
DB 50 DINPNNGGTSYNQKFKG 66

RESULT 10
ATOS_ECOLI STANDARD; PRT; 608 AA.
AC Q06067;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sensor protein atos (EC 2.7.3.-).
GN AOS OR B2219.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=93348226; PubMed=8346225;
RA Canellakis E.S., Paterakis A.A., Huang S.-C., Panagiotidis C.A.,
RA Kyriakidis D.A.;
RT "Identification, cloning, and nucleotide sequencing of the ornithine
decarboxylase antizyme gene of Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:7129-7133(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sempel G., Seki Y., Sivasubram S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Diidrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

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Glickman A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
Tucker P.W.;
"illegitimate recombination generates a class switch from C mu to C
delta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
PIR: A02033; HVMS7.
HSSP: P01810; 2FBJ.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_V.
Pfam: PF00047; Ig; 1.
SMART; SM00406; Igv; 1.
Immunoglobulin V region; Signal.
SIGNA 1 20
CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
DOMAIN 21 49 FRAMEWORK-1.
DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
DOMAIN 55 68 FRAMEWORK-2.
DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
DOMAIN 86 117 FRAMEWORK-3.
DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
DOMAIN 128 138 FRAMEWORK-4.
DISULFID 41 115 BY SIMILARITY.
NON_TER 138 138
SEQUENCE 138 AA: 15576 MW: 748157E4C6907B8E CRC64;

Query Match 48.9%; Score 46; DB 1; Length 138;
Best Local Similarity 56.2%; Pred. No. 1.4;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 EITYPGSGSYNNEMFK 16
|| | : ||| ||
DB 69 EINPDGRSGSYNEKFK 84

RESULT 12
HV05_MOUSE
ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 21-JUL-1986 (Rel. 01, Last annotation update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 3 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6;
MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Faskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
"Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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EMBL; J00536; AAA38605.1; -.
PIR: A02031; HVMS3.
HSSP: P01810; 2FBJ.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_V.
Pfam: PF00047; Ig; 1.
SMART; SM00406; Igv; 1.

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KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 50 54 FRAMEWORK-1
FT DOMAIN 55 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

Query Match 47.9%; Score 45; DB 1; Length 117;
Best Local Similarity 46.7%; Pred. No. 1.7;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IYPGSGSAYINEMFK 16
DB 70 IYPSDSETHYNQFK 84
:::|::|::|

JULT 13
5_PICPA
ID PEX5_PICPA STANDARD; PRT; 576 AA.
AC P33292; Q01967;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Peroxisomal targeting signal receptor (Peroxisomal protein PAS8)
DE (Peroxin-5) (PTSI receptor).
GN PEX5 OR PAS8.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-11430;
RX MEDLINE=93260010; PubMed=8098333;
RA McCollum D., Monosov E., Subramani S.;
RT "The pas8 mutant of Pichia pastoris exhibits the peroxisomal protein
RT import deficiencies of Zellweger syndrome cells -- the PAS8 protein
RT binds to the COOH-terminal tripeptide peroxisomal targeting signal,
RT and is a member of the TPR protein family";
RT J. Cell Biol. 121:761-774(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Gould S.J., Kalish J.E., Morrel J.C., Bjorkman J., Urquhart A.J.,
RA Crane D.I.;
RA Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
FUNCTION.
RX MEDLINE=95369234; PubMed=7641682;
RA Terlecky S.R., Nuttle W.M., McCollum D., Sock E., Subramani S.;
RT "The Pichia pastoris peroxisomal protein PAS8p is the receptor for
RT the C-terminal tripeptide peroxisomal targeting signal";
RL EMBO J. 14:3627-3634(1995).
CC -!- FUNCTION: BINDS TO THE C-TERMINAL PTSI-TYPE TRIPEPTIDE PEROXISOMAL
CC TARGETING SIGNAL (SKL-TYPE) AND PLAYS AN ESSENTIAL ROLE IN
CC PEROXISOMAL PROTEIN IMPORT.
CC -!- SUBCELLULAR LOCATION: ITS DISTRIBUTION APPEARS TO BE DYNAMIC. IT
CC IS PROBABLY A CYCLING RECEPTOR FOUND MAINLY IN THE CYTOPLASM AND
CC AS WELL ASSOCIATED TO THE PEROXISOMAL MEMBRANE THROUGH A DOCKING
CC FACTOR (PEX13).
CC -!- SIMILARITY: CONTAINS 7 TPR REPEATS.
CC -!- SIMILARITY: STRONG, TO OTHER PEROXISOMAL TARGETING SIGNAL
CC RECEPTORS.

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CC EMBL; Z19592; CAA79640.1; -
CC EMBL; U59222; AAB40613.1; -
CC PIR; A40688; A40688.
CC InterPro: IPR001440; TPR.
CC Pfam; PF00515; TPR; 4.
CC SMART; SM00028; TPR; 4.
KW Peroxisome; Repeat; TPR repeat; Transport; Protein transport.
FT DOMAIN 19 232 GLN-RICH.
FT REPEAT 278 311 TPR 1.
FT REPEAT 312 345 TPR 2.
FT REPEAT 346 383 TPR 3.
FT REPEAT 384 421 TPR 4.
FT REPEAT 422 455 TPR 5.
FT REPEAT 456 489 TPR 6.
FT REPEAT 490 523 TPR 7.
FT CONFLICT 243 259 DQFAQWEKDFQAQYAE -> RPVSGSGMGERFCPIRRR
FT (IN REF. 1).
SQ SEQUENCE 576 AA; 65083 MW; C249FBES0FDE5247 CRC64;

Query Match 47.9%; Score 45; DB 1; Length 576;
Best Local Similarity 46.7%; Pred. No. 9.5;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELYPGSGSAYINEMF 15
DB 560 KVPYGMGLAQFRKM 574
:::|::|::|::|

RESULT 14
VGL2_CVHOC
ID VGL2_CVHOC STANDARD; PRT; 1353 AA.
AC P36334;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE E2 glycoprotein precursor (Spike glycoprotein) (Peplomer protein)
DE [Contains: Spike protein S1 (90B); Spike protein S2 (90A)].
GN S.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=31631;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93389458; PubMed=8376972;
RA Mounir S., Talbot P.J.;
RT "Molecular characterization of the S protein gene of human
RT coronavirus OC43";
RL J. Gen. Virol. 74:1981-1987(1993).
CC -!- FUNCTION: THE PEPLIMER PROTEIN MEDIATES THE BINDING OF VIRIONS
CC TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION
CC AND IN SYNCYTUM FORMATION.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

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CC EMBL; L14643; AAA03055.1; -
CC PIR; JQ2168; JQ2168.
CC InterPro: IPR002552; Corona_S2.
CC Pfam; PF01601; Corona_S2; 1.
KW Glycoprotein; Envelope protein; Transmembrane; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 1353 E2 GLYCOPROTEIN.
FT CHAIN 18 757 SPIKE PROTEIN S1.

FT CHAIN 758 1353 SPIKE PROTEIN S2. (POTENTIAL).
FT DOMAIN 18 1298 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1299 1318 POTENTIAL.
FT DOMAIN 1319 1353 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1319 1336 CYS-RICH.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 496 496 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 639 639 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 666 666 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 686 686 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 704 704 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 729 729 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 778 778 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 927 927 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1184 1184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1214 1214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1224 1224 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1243 1243 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1257 1257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1278 1278 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1353 AA; 150088 MW; 781CE3CDBD1A902A CRC64;
Query Match 47.9%; Score 45; DB 1; Length 1353;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 YPGSGSAYYNEMFKG 17
DB 68 YPTSGSTYRNALKG 82
RESULT 15
VGL2_CVBF STANDARD; PRT; 1363 AA.
ID VGL2_CVBF
AC P25190;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE E2 glycoprotein precursor (Spike glycoprotein) (Peplover protein)
DE [Contains: Spike protein S1 (90B); Spike protein S2 (90A)].
GN S.
BO Bovine coronavirus (strain F15).
VIR Viruses; ssRNA positive-strand viruses, no DNA stage: Nidovirales;
COR Coronaviridae; Coronavirus.
OX NCBI_TaxID=11129;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90171938; PubMed=2155300;
RX Boireau P., Cruciere C., Laporte J.;
RT "Nucleotide sequence of the glycoprotein S gene of bovine enteric
RT coronavirus and comparison with the S proteins of two mouse hepatitis
RT virus strains".
RL J. Gen. Virol. 71:487-492(1990).
CC -!- FUNCTION: THE PELOMER PROTEIN MEDIATES THE BINDING OF VIRIONS
CC TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
CC -----
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CC -----
CC EMBL; D00731; BAA0631.1; -.
DR PIR; A34151; VGIHF1.
DR InterPro; IPR002552; Corona_S2.
DR Pfam; PF01601; Corona_S2; 1.

KW Glycoprotein; Envelope protein; Transmembrane; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 1363 E2 GLYCOPROTEIN.
FT CHAIN 18 768 SPIKE PROTEIN S1.
FT CHAIN 769 1363 SPIKE PROTEIN S2.
FT DOMAIN 18 1311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1312 1328 POTENTIAL.
FT DOMAIN 1329 1363 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1329 1346 CYS-RICH.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 676 676 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 696 696 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 714 714 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 739 739 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 788 788 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 937 937 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1194 1194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1224 1224 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1234 1234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1253 1253 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1267 1267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1288 1288 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1363 AA; 150746 MW; 3245CD74D70AD135 CRC64;
Query Match 47.9%; Score 45; DB 1; Length 1363;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 YPGSGSAYYNEMFKG 17
DB 68 YPTSGSTYRNALKG 82
Search completed: February 14, 2003, 11:16:20
Job time : 9.77419 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:10:17 : Search time 35,371 Seconds
(without alignments)
99.030 Million cell updates/sec

Title: US-09-701-001b-2
Perfect score: 94
Sequence: 1 E1YPGSGSAYYNEMFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Search: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.rodent.*
- 12: sp.virus.*
- 13: sp.vertebrate.*
- 14: sp.unclassified.*
- 15: sp.rvirus.*
- 16: sp.bacteriaph.*
- 17: sp.archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	76	80.9	463	11 Q99LC4	Q99LC4 mus musculus
2	70	74.5	473	11 Q9D8L4	Q9D8L4 mus musculus
3	68	72.3	110	11 Q9JL83	Q9JL83 mus musculus
4	67	71.3	613	11 Q8VCX7	Q8VCX7 mus musculus
5	66	70.2	143	11 Q9D4Q0	Q9D4Q0 mus musculus
6	63	67.0	481	11 Q91WT1	Q91WT1 mus musculus
7	62	66.0	147	11 Q92S53	Q92S53 mus musculus
8	62	66.0	168	11 Q8VDC9	Q8VDC9 mus musculus
9	59	62.8	110	11 Q9JL77	Q9JL77 mus musculus
10	58	61.7	473	11 Q99L25	Q99L25 mus musculus
11	55	58.5	111	11 Q9D9B8	Q9D9B8 mus musculus
12	50	53.2	118	11 Q9Z1C4	Q9Z1C4 mus musculus
13	50	53.2	335	16 Q9WXS7	Q9WXS7 thermotoga
14	48	51.1	121	16 Q8YL22	Q8YL22 anabaena sp
15	48	51.1	372	2 Q9F6B4	Q9F6B4 campylobact
16	48	51.1	489	11 Q8VCX4	Q8VCX4 mus musculus

17	47	50.0	117	11 Q9QXF0	Q9QXF0 mus musculus
18	47	50.0	117	11 Q9QXE9	Q9QXE9 mus musculus
19	47	50.0	187	8 Q9TCB6	Q9TCB6 nephroselmi
20	47	50.0	373	9 Q9AZR7	Q9AZR7 bacterioph
21	47	50.0	373	16 Q9CFT0	Q9CFT0 lactococcus
22	46	48.9	474	11 Q8R3H6	Q8R3H6 mus musculus
23	45	47.9	278	11 Q921K1	Q921K1 mus musculus
24	45	47.9	373	9 Q80182	Q80182 streptococ
25	45	47.9	373	9 Q34074	Q34074 streptococ
26	45	47.9	768	12 Q9DR83	Q9DR83 bovine coro
27	45	47.9	768	12 Q9DR82	Q9DR82 bovine coro
28	45	47.9	768	12 Q99H68	Q99H68 bovine coro
29	45	47.9	768	12 Q9DR80	Q9DR80 bovine coro
30	45	47.9	768	12 Q99S26	Q99S26 bovine coro
31	45	47.9	768	12 Q99AS7	Q99AS7 bovine coro
32	45	47.9	768	12 Q65396	Q65396 bovine coro
33	45	47.9	791	12 Q99134	Q99134 bovine coro
34	45	47.9	1361	12 Q66199	Q66199 human coron
35	45	47.9	1361	12 Q86623	Q86623 human coron
36	45	47.9	1363	12 Q66290	Q66290 human coron
37	45	47.9	1363	12 Q66291	Q66291 human coron
38	45	47.9	1363	12 Q9QAR5	Q9QAR5 bovine coro
39	45	47.9	1363	12 Q9QA08	Q9QA08 bovine coro
40	45	47.9	1363	12 Q91A26	Q91A26 bovine coro
41	45	47.9	1363	12 Q8V436	Q8V436 bovine coro
42	44	46.8	137	11 Q924R6	Q924R6 mus musculus
43	44	46.8	139	11 Q924R5	Q924R5 mus musculus
44	44	46.8	140	11 Q924R2	Q924R2 mus musculus
45	44	46.8	141	11 Q924Q4	Q924Q4 mus musculus

ALIGNMENTS

RESULT 1

ID	Q99LC4	PRELIMINARY;	PRT;	463 AA.
AC	Q99LC4;			
DT	01-JUN-2001 (TrEMBLrel. 17, Created)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Similar to RIKEN cDNA 1810060009 gene.			
GN	IGH-4.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Strausberg R.;			
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC003435; AA03435.1; -			
DR	HSSP; P01842; 7FAB.			
DR	MGD; MGI:96446; Igh-4.			
DR	InterPro; IPR003599; Igh-4.			
DR	InterPro; IPR003597; Igh-cl.			
DR	InterPro; IPR003600; Igh-like.			
DR	InterPro; IPR003006; Igh_MHC.			
DR	InterPro; IPR003596; Igh_v.			
DR	Pfam; PF00047; Igh; 4.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGcl; 2.			
DR	SMART; SM00406; IGV; 1.			
DR	SMART; SM00410; IG-like; 1.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.			
SQ	SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;			

Query Match 80.9%; Score 76; DB 11; Length 463;
Best Local Similarity 76.5%; Pred. No. 0.00047;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 E1YPGSGSAYYNEMFKG 17
|||||||:|:|:|

Db 69 E1YPGSGNTYYSEKFG 85

RESULT 2

Q9D8L4 PRELIMINARY; PRT; 473 AA.
 ID Q9D8L4
 AC Q9D8L4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 181006009Rik protein.
 GN IGH-1 OR 181006009RIK.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Rono H., Baldarelli R., Barsh G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 Hayashizaki Y.;
 RT Functional annotation of a full-length mouse cDNA collection.;
 RL Nature 409:685-690 (2001).
 DR EMBL; AK007918; BAB25349.1; .
 DR HSSP; P01842; 7FAB.
 DR MGD; MGI:96443; Igh-1.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003600; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; Igc1; 3.
 DR SMART; SM00406; Igv; 1.
 DR SMART; SM00410; Ig-like; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 SQ SEQUENCE 473 AA; 51699 MW; 9DE57A514475FEB CRC64;

Query Match 74.5%; Score 70; DB 11; Length 473;
 Best Local Similarity 76.5%; Pred. No. 0.0045;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 E1YPGSGSAYNEMFKG 17

:|||||

Db 69 K1PGSGSNTYYNEKFG 85

RESULT 3

Q9JL83 PRELIMINARY; PRT; 110 AA.
 ID Q9JL83
 AC Q9JL83;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Anti-myosin immunoglobulin heavy chain variable region

DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=20448942; PubMed=10992488;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "T-Cell-dependent antibody response to the dominant epitope of
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 RL with cardiac myosin.";
 RL Infect. Immun. 68:5803-5808 (2000).
 DR EMBL; AF206023; AAF69321.1; .
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 FT NON_TER 1
 FT NON_TER 110 110
 SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match 72.3%; Score 68; DB 11; Length 110;
 Best Local Similarity 75.0%; Pred. No. 0.0019;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGSGSAYNEMFKG 17

|||||

Db 43 IYPGSGDAYNGKFG 58

RESULT 4

Q8VCX7 PRELIMINARY; PRT; 613 AA.
 ID Q8VCX7
 AC Q8VCX7;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 67.9 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary Gland;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC018315; AAH18315.1; .
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; Igc1; 4.
 DR SMART; SM00406; Igv; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 71.3%; Score 67; DB 11; Length 613;
 Best Local Similarity 76.5%; Pred. No. 0.019;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 E1YPGSGSAYNEMFKG 17

|||||

Db 69 E1LPGSGSNTYYNEKFG 85

RESULT 5

Q924Q0 PRELIMINARY; PRT; 143 AA.

Q924Q0: 01-DEC-2001 (TrEMBLrel. 19, Created)

01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

V165-D-J-C mu protein (Fragment).

V165-D-J-C MU.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

STRAIN=C57BL/6;

Kozono Y., Kozono H., Azuma T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals

Affinity Maturation of B Cell Antigen Receptors in Response to (4-

Hydroxy-3-Nitrophenyl)Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

EMBL; AB069915; BAB63931.1; "

InterPro; IPR003006; Ig_MHC.

Pfam; PF00047; Ig; 1.

NON_TER 1

NON_TER 143 143

SEQUENCE 143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;

Query Match 70.2%; Score 66; DB 11; Length 143;

Best Local Similarity 75.0%; Pred. No. 0.0054;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIIYPGSGSAYYNEMFK 16

DB 50 DIIYPGSGSTNYNEKFK 65

RESULT 6

Q91WT1 PRELIMINARY; PRT; 481 AA.

AC Q91WT1 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Hypothetical 52.1 kDa protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

TISSUE=COLON;

RA Strausberg R.;

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; BC013490; AAH13490.1; "

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

KW Hypothetical protein.

SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 67.0%; Score 63; DB 11; Length 481;

Best Local Similarity 68.8%; Pred. No. 0.063;

Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEMFKG 17

DB 70 IYPGDGTNYNEKFKG 85

RESULT 7

Q925S3 PRELIMINARY; PRT; 147 AA.

ID Q925S3

AC Q925S3;

SQ SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;

Query Match 66.08; Score 62; DB 11; Length 168;
Best Local Similarity 70.68; Pred. No. 0.029;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 E1YPGSGSAYYNEMFKG 17

Db 69 E1LPGSGRTNNEKFKG 85

RESULT 9

Q9JL77 PRELIMINARY; PRT; 110 AA.

AC Q9JL77
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region (Fragment).
DE OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206029; AAF69327.1; -
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 12138 MW; 2ED81PF5862C9AF CRC64;

Query Match 62.8%; Score 59; DB 11; Length 110;
Best Local Similarity 64.7%; Pred. No. 0.055;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 E1YPGSGSAYYNEMFKG 17

Db 42 E1RPNSGHTNNEKFKG 58

RESULT 10

Q9JL25 PRELIMINARY; PRT; 473 AA.

AC Q9JL25
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE Similar to RIKEN cdna 181060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AA003888.1; -
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.

DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 61.7%; Score 58; DB 11; Length 473;
Best Local Similarity 68.8%; Pred. No. 0.41;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEMFKG 17

Db 70 IYPRDGTSTYNEKFKG 85

RESULT 11

Q9D9B8 PRELIMINARY; PRT; 111 AA.

AC Q9D9B8
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Adult male testis cDNA, RIKEN full-length enriched library, clone:170011011, full insert sequence.
DE OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I., Saito I., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ra Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Schirml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Gustincich S., Hill D., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Nordone P., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Sasaki H., Toyo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007163; BAB24877.1; -
DR HSSP; P01810; 2FBJ
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
SQ SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;

Query Match 58.5%; Score 55; DB 11; Length 111;
Best Local Similarity 62.5%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEMFKG 17

SQ SEQUENCE 372 AA; 4 2290 MW; 695CDBDE4DZFL116 CRC64;

DR IIGK; IM0072; BPD_transp.
DR Interpro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp; 1.

Query Match 51.1%; Score 48; DB 2; Length 372;
 Best Local Similarity 45.5%; Pred. No. 13;
 Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 1;

QY 1 EYPCSGSA-----YYNEMFK 16
 ||| | :| ||| :||
 Db 100 EYKGEANASISIKYNDLFK 121

Search completed: February 14, 2003, 11:18:37
 Job time : 36.5376 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run On: February 14, 2003, 11:04:17 ; Search time 24.3871 Seconds
(without alignments)
49.176 Million cell updates/sec

Title: US-09-701-001b-3
Perfect score: 50
Sequence: 1 RGTGTGFAY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Search: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	9	21	Antibody 4H5 H cha
2	50	100.0	9	21	Murine CD4/CD34 re
3	50	100.0	110	21	Antibody 4H5 H cha
4	50	100.0	110	21	Murine derived pro
5	50	100.0	118	21	Antibody 4H5 H cha
6	50	100.0	118	21	Murine derived pro
7	50	100.0	118	21	Murine derived pro
8	50	100.0	305	21	Antibody 4H5 H cha
9	50	100.0	305	21	Antibody 4H5 L cha
10	50	100.0	305	21	Murine derived pro

11	50	100.0	305	21	AAV51142
12	44	88.0	20	23	AAU70801
13	44	88.0	130	23	AAU70768
14	40	80.0	122	11	AAU04135
15	40	80.0	136	11	AAU04133
16	39	78.0	176	22	AAU19301
17	37	74.0	21	21	AAV51684
18	37	74.0	219	21	AAV51679
19	37	74.0	266	22	AAU60366
20	36	72.0	150	23	ABU77826
21	35	70.0	145	20	AAU48329
22	35	70.0	177	22	AAU67760
23	35	70.0	277	20	AAU96343
24	35	70.0	338	23	ABU41394
25	35	70.0	439	22	ABU76766
26	35	70.0	448	22	AAU93041
27	35	70.0	576	21	AAU54335
28	35	70.0	579	14	AAU34446
29	35	70.0	579	14	AAU34401
30	35	70.0	640	20	AAU39926
31	35	70.0	789	23	ABU05687
32	34	68.0	94	22	AAU83608
33	34	68.0	105	21	AAU20186
34	34	68.0	105	21	AAU47232
35	34	68.0	134	21	AAU20185
36	34	68.0	134	21	AAU47231
37	34	68.0	163	21	AAU38045
38	34	68.0	251	20	AAU88496
39	34	68.0	251	21	AAU41852
40	34	68.0	251	21	AAU66632
41	34	68.0	251	22	AAU29024
42	34	68.0	251	22	AAU78501
43	34	68.0	251	22	AAU65155
44	34	68.0	277	19	AAU85849
45	34	68.0	279	20	AAU60100

ALIGNMENTS

RESULT 1
AAV59258
ID AAV59258 standard; peptide: 9 AA.
XX
AC AAV59258;
XX
DT 17-APR-2000 (first entry)
XX
DE Antibody 4H5 H chain variable region CDR3 fragment.
XX
XX CD4 antigen; anti-human; antibody: 4H5; drug: CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
XX JP1132563-A.
XX
PD 07-DEC-1999.
XX
XX 26-MAY-1998; 98JP-0163034.
XX
XX 26-MAY-1998; 98JP-0163034.
XX
XX (ASAH) ASAH KASEI KOGYO KK.
XX
XX WPI; 2000-091351/08.
XX
XX An antibody and the nucleic acid coding the antibody -
XX
XX Claim 1; Page 14; 25pp; Japanese.
XX
XX The invention provides an antibody having affinity to CD4 antigen. The
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and

Murine derived pro
Hepatitis B virus
Hepatitis B virus
Anti-Leu 3a heavy
Anti-Leu 3a heavy
Human G protein-co
Murine clodin 3 pr
zebrafish atonal h
Amino acid sequenc
Human prostate can
Propionibacterium
sfvMHC-1-8k single
Human ovarian anti
Corynebacterium gl
C glutamic prote
Human pancreatic c
N.meningitidis 239
Sequence of low mo
Bovine rotavirus S
Human differentiat
Human immune/haema
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Fragment of human
Human stomach canc
Human ORFX ORF1616
Membrane-bound pro
Human PRO polypept
Human protein SEQ
Human PRO276 (UNQ2
S. pneumoniae deri
Human endometrium

CC application for drugs. It is highly safe in human dose. Sequences
 CC AAY59256-58 represent the complementarity determining region (CDR)-L,
 CC CDR-2 and CDR-3 fragments in the H chain variable region of the
 CC antibody 4H5 respectively.
 XX
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9
 |||||
 Db 1 RGTGTGFAY 9

RESULT 2

AAAY51135
 XX AAY51135 standard; Protein; 9 AA.

AC AAY51135;

31-MAR-2000 (first entry)

DE Murine CD4/CD34 recognizing antibody heavy chain CDR-3 region #1.

KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; complementarity determining region;
 KW CDR-3; heavy chain; murine.

OS Mus sp.

XX WO9961629-A1.

XX 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711.

XX 25-MAY-1998; 98JP-0159957.

XX 26-MAY-1998; 98JP-0163023.

XX (ASAH) ASAHI KASEI KOGYO KK.

XX (ASAH) ASAHI MEDICAL CO LTD.

XX Ono M, Soka T, Morimoto I, Miyamura K;

XX WPI; 2000-086720/07.

XX Devices containing antibodies recognising CD4 or CD34 and their use for
 the separation of CD4 or CD34 positive cells -

PS Claim 3; Page 76; 11pp; Japanese.

CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived complementarity determining
 CC region CDR-3 protein fragment which is used to illustrate the method of
 CC the invention.

SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9

Db 1 RGTGTGFAY 9

RESULT 3

AAAY59262

XX AAY59262 standard; protein; 110 AA.

XX AAY59262;

XX 17-APR-2000 (first entry)

XX Antibody 4H5 H chain variable region.

XX CD4 antigen; anti-human; antibody; 4H5; drug.

XX Mus sp.

XX JP11332563-A.

XX 07-DEC-1999.

XX 26-MAY-1998; 98JP-0163034.

XX 26-MAY-1998; 98JP-0163034.

XX (ASAH) ASAHI KASEI KOGYO KK.

XX WPI; 2000-091351/08.

XX N-PSDB; AAZ58661.

XX An antibody and the nucleic acid coding the antibody -

XX Claim 5; Page 15; 25pp; Japanese.

CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the H chain variable region of the antibody 4H5.

SQ Sequence 110 AA;

Query Match 100.0%; Score 50; DB 21; Length 110;

Best Local Similarity 100.0%; Pred. No. 0.42;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9

|||||

Db 91 RGTGTGFAY 99

RESULT 4

AAAY51139

XX AAY51139 standard; Protein; 110 AA.

XX AAY51139;

XX 31-MAR-2000 (first entry)

XX Murine derived protein fragment #1.

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;

XX hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;

XX HIV infection; autoimmune disease; murine.

XX Mus sp.

XX WO9961629-A1.

XX 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711.

put priority for withdrawal

XX	Sequence	118 AA;
XX	Query Match	100.0%; Score 50; DB 21; Length 118;
XX	Best Local Similarity	100.0%; Pred. No. 0.45; Mismatches 9; Conservative 0; Indels 0; Gaps 0;
QY	1 RGTGTFAY 9	
DB	99 RGTGTFAY 107	
XX	AAAY51143;	
XX	AC	
XX	XX	
DE	31-MAR-2000 (first entry)	
XX	Murine derived protein fragment #5.	
XX	Cluster differentiation: cell separation; antibody; CD4; CD34; leukemia;	
KW	hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;	
KW	HIV infection; autoimmune disease; murine.	
XX	Mus sp.	
OS	WO9961629-A1.	
PN	02-DEC-1999.	
PD	24-MAY-1999; 99WO-JP02711.	
XX	25-MAY-1998; 98JP-0159957.	
PR	26-MAY-1998; 98JP-0163023.	
XX	(ASAH) ASAH KASEI KOGYO KK.	
PA	(ASAH) ASAH MEDICAL CO LTD.	
XX	Ono M, Soka T, Morimoto I, Miyamura K;	
PI	WPI; 2000-086720/07.	
XX	Devices containing antibodies recognising CD4 or CD34 and their use for	
XX	the separation of CD4 or CD34 positive cells -	
PT	Disclosure; Page 94-95; lllpp: Japanese.	
PS	This invention describes a novel device (I) for separating cluster	
XX	differentiation (CD)-positive cells using a recombinant (chimeric or	
CC	single-chain) antibody recognising CD4 or CD34. The devices are useful	
CC	for the separation of CD4 or CD34 positive cells, which is useful for	
CC	the collection of hematopoietic undifferentiated cells, elimination of	
CC	lymphocytes from cells to be used in bone marrow transplantation, the	
CC	detection of leukemic cells and the production of medicinal	
CC	compositions for the treatment of HIV infection and autoimmune diseases.	
CC	This sequence represents a murine derived protein fragment which is used	
CC	to illustrate the method of the invention.	
XX	Sequence	118 AA;
XX	Query Match	100.0%; Score 50; DB 21; Length 118;
XX	Best Local Similarity	100.0%; Pred. No. 0.45; Mismatches 9; Conservative 0; Indels 0; Gaps 0;
QY	1 RGTGTFAY 9	
DB	99 RGTGTFAY 107	
XX	AAAY51145	
XX	RESULT 7	

ID AAY51145 standard; Protein: 118 AA.
 AC AAY51145;
 XX 31-MAR-2000 (first entry)
 DT Murine derived protein fragment #7.
 XX
 DE Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 XX hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 XX
 OS Mus sp.
 XX
 PN WO9961629-A1.
 XX
 PD 02-DEC-1999.
 XX
 PF 24-MAY-1999; 99WO-JP02711.
 XX
 PR 25-MAY-1998; 98JP-0159957.
 XX
 PR 26-MAY-1998; 98JP-0163023.
 XX
 (ASAH) ASAH KASEI KOGYO KK.
 PA (ASAH) ASAH MEDICAL CO LTD.
 PI Ono M, Soka T, Morimoto I, Miyamura K;
 XX
 DR WPI; 2000-086720/07.
 DR N-PSDB; AAZ44231.
 XX
 PT Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells
 XX
 XX Disclosure; Page 96-97; 111pp; Japanese.
 XX
 CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 XX
 SQ Sequence 118 AA;
 Query Match 100.0%; Score 50; DB 21; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.45; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGTGTGFAY 9
 DB 99 RGTGTGFAY 107
 RESULT 8
 AAY59264
 ID AAY59264 standard; protein; 305 AA.
 XX
 AC AAY59264;
 XX
 DT 17-APR-2000 (first entry)
 XX
 DE Antibody 4H5 H chain sequence.
 XX
 KW CD4 antigen; anti-human; antibody; 4H5; drug.
 XX
 OS Mus sp.
 XX
 PN JP11332563-A.
 XX
 DR WPI; 2000-091351/08.
 DR N-PSDB; AAZ58664.
 XX
 PT An antibody and the nucleic acid coding the antibody -
 PT Disclosure; Page 17-18; 25pp; Japanese.
 PS
 XX The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the L chain sequence of the antibody 4H5.
 CC
 XX Sequence 305 AA;
 Query Match 100.0%; Score 50; DB 21; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGTGTGFAY 9
 DB 247 RGTGTGFAY 255
 RESULT 9
 AAY59265
 ID AAY59265 standard; protein; 305 AA.
 XX
 AC AAY59265;
 XX
 DT 17-APR-2000 (first entry)
 XX
 DE Antibody 4H5 L chain sequence.
 XX
 KW CD4 antigen; anti-human; antibody; 4H5; drug.
 XX
 OS Mus sp.
 XX
 PN JP11332563-A.
 XX
 DR 07-DEC-1999.
 XX
 PF 26-MAY-1998; 98JP-0163034.
 XX
 PR 26-MAY-1998; 98JP-0163034.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 DR WPI; 2000-091351/08.
 DR N-PSDB; AAZ58664.
 XX
 PT An antibody and the nucleic acid coding the antibody -
 PT Disclosure; Page 17-18; 25pp; Japanese.
 PS
 XX The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the L chain sequence of the antibody 4H5.
 CC
 XX Sequence 305 AA;
 Query Match 100.0%; Score 50; DB 21; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGTGTGFAY 9
 DB 247 RGTGTGFAY 255

XX 07-DEC-1999.
 PD 26-MAY-1998; 98JP-0163034.
 XX 26-MAY-1998; 98JP-0163034.
 PR (ASAH) ASAH KASEI KOGYO KK.
 PA WPI; 2000-091351/08.
 XX N-PSDB; AAZ58663.
 DR
 XX An antibody and the nucleic acid coding the antibody -
 PT Disclosure; Page 16-17; 25pp; Japanese.
 PS
 XX The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the H chain sequence of the antibody 4H5.
 CC
 XX Sequence 305 AA;
 Query Match 100.0%; Score 50; DB 21; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGTGTGFAY 9
 DB 247 RGTGTGFAY 255
 RESULT 9
 AAY59265
 ID AAY59265 standard; protein; 305 AA.
 XX
 AC AAY59265;
 XX
 DT 17-APR-2000 (first entry)
 XX
 DE Antibody 4H5 L chain sequence.
 XX
 KW CD4 antigen; anti-human; antibody; 4H5; drug.
 XX
 OS Mus sp.
 XX
 PN JP11332563-A.
 XX
 DR 07-DEC-1999.
 XX
 PF 26-MAY-1998; 98JP-0163034.
 XX
 PR 26-MAY-1998; 98JP-0163034.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 DR WPI; 2000-091351/08.
 DR N-PSDB; AAZ58664.
 XX
 PT An antibody and the nucleic acid coding the antibody -
 PT Disclosure; Page 17-18; 25pp; Japanese.
 PS
 XX The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the L chain sequence of the antibody 4H5.
 CC
 XX Sequence 305 AA;
 Query Match 100.0%; Score 50; DB 21; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGTGTGFAY 9
 DB 247 RGTGTGFAY 255

OY 1 RGTGTGFAY 9
|||||
DB 121 RGTGTGFAY 129

RESULT 10
AA51141
ID AA51141 standard; Protein; 305 AA.

XX AC
XX AAY51141;
XX
DT 31-MAR-2000 (first entry)

XX Murine derived protein fragment #3.

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
HIV infection; autoimmune disease; murine.

OS Mus sp.

XX WO9961629-A1.

XX 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711.

XX 25-MAY-1998; 98JP-0159957.

XX 26-MAY-1998; 98JP-0163023.

XX (ASAH) ASAH KASEI KOGYO KK.

XX (ASAH) ASAH MEDICAL CO LTD.

XX Ono M, Soka T, Morimoto I, Miyamura K;

XX WPI; 2000-086720/07.

XX N-PSDB; AA244205.

XX Devices containing antibodies recognising CD4 or CD34 and their use for
PT the separation of CD4 or CD34 positive cells

XX Claim 22; Page 80-82; 111pp; Japanese.

XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for
XX the collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal
XX compositions for the treatment of HIV infection and autoimmune diseases.
XX This sequence represents a murine derived protein fragment which is used
XX to illustrate the method of the invention.

XX Sequence 305 AA;

Query Match 100.0%; Score 50; DB 21; Length 305;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGTGTGFAY 9

|||||

DB 247 RGTGTGFAY 255

RESULT 11

AA51142

ID AA51142 standard; Protein; 305 AA.

XX AC AAY51142;

XX 31-MAR-2000 (first entry)

XX

DE Murine derived protein fragment #4.

XX

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; murine.

XX Mus sp.

XX WO9961629-A1.

XX 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711.

XX 25-MAY-1998; 98JP-0159957.

XX 26-MAY-1998; 98JP-0163023.

XX (ASAH) ASAH KASEI KOGYO KK.

XX (ASAH) ASAH MEDICAL CO LTD.

XX Ono M, Soka T, Morimoto I, Miyamura K;

XX WPI; 2000-086720/07.

XX N-PSDB; AA244205.

XX Devices containing antibodies recognising CD4 or CD34 and their use for
PT the separation of CD4 or CD34 positive cells

XX Claim 22; Page 82-84; 111pp; Japanese.

XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for
XX the collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal
XX compositions for the treatment of HIV infection and autoimmune diseases.
XX This sequence represents a murine derived protein fragment which is used
XX to illustrate the method of the invention.

XX Sequence 305 AA;

Query Match 100.0%; Score 50; DB 21; Length 305;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGTGTGFAY 9

|||||

DB 121 RGTGTGFAY 129

RESULT 12

AAU70801

ID AAU70801 standard; Peptide; 20 AA.

XX AC AAU70801;

XX 14-FEB-2002 (first entry)

XX Hepatitis B virus antigen binding partner #33.

XX Hepatitis B virus; virucide; immunomodulator; hepatotropic; HBV;

XX anti-inflammatory; HBV core antigen; HBcAg; HBV E antigen; HBeAg;

XX B cell mediated processing; T cell proliferation; cytokine production;

XX immune system response.

XX Synthetic.

XX WO200181421-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-IB00844.
 XX 21-APR-2000; 2000US-0556605.
 XX (TRIP-) TRIPEP AB.
 XX Sallberg M;
 XX WPI; 2002-055347/07.
 XX Novel peptide that binds to hepatitis B virus core or E antigen, useful
 XX for treating and preventing hepatitis B virus infection -
 XX Claim 2; Page 33; 82pp; English.
 XX The invention relates to an isolated or purified peptide (I) which binds
 XX Hepatitis B virus (HBV) core antigen (HBcAg) or HBV E antigen (HBeAg).
 XX (I) is useful for treating or preventing Hepatitis B virus (HBV)
 XX infection, by identifying a subject in need of a molecule that inhibits
 XX HBV infection, and providing the subject with (I). (I) is also useful
 XX for determining the presence of HBV in a biological sample, and for
 XX inhibiting B cell mediated processing and uptake of HBcAg and/or HBeAg,
 XX by determining whether (I) inhibits B cell mediated processing and
 XX uptake of HBcAg and/or HBeAg by performing an assay of T cell
 XX proliferation or cytokine production. (I) is also useful for modulating
 XX an immune system response. (I) is useful as a template for a design of
 XX synthetic molecules including peptides, derivatives or modified peptides,
 XX peptidomimetics and chemicals. (I) is also useful as biotechnological
 XX tool, diagnostic reagent and as active ingredient in pharmaceuticals.
 XX (I) is also useful as detection reagents in conventional
 XX immunohistochemical techniques, as diagnostic reagents to detect HBV in
 XX biological sample, and to determine the efficacy of an HBV treatment
 XX protocol by monitoring the levels of HBcAg and/or HBeAg during and after
 XX treatment. AAU70766-AAU70876 represent Hepatitis B virus (HBV) core
 XX antigen (HBcAg) or HBV E antigen (HBeAg) binding partners as described
 XX in the invention.
 XX Sequence 20 AA;
 SQ Query Match 88.0%; Score 44; DB 23; Length 20;
 Best Local Similarity 88.9%; Pred. No. 0.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RGTGTGFAY 9
 Db 7 RGKGTGFAY 15
 RESULT 13
 0768
 AAU70768 standard; Peptide; 130 AA.
 XX AAU70768;
 AC AAU70768;
 XX 14-FEB-2002 (first entry)
 DT Hepatitis B virus antigen binding partner 9C8 VH.
 DE Hepatitis B virus; virucide; immunomodulator; hepatotropic; HBV;
 KW antinflammatory; HBV core antigen; HBcAg; HBV E antigen; HBeAg;
 KW B cell mediated processing; T cell proliferation; cytokine production;
 KW immune system response.
 XX Synthetic.
 OS WO200181421-A2.
 PN 01-NOV-2001.
 XX 20-APR-2001; 2001WO-IB00844.
 XX 21-APR-2000; 2000US-0556605.

XX (TRIP-) TRIPEP AB.
 XX Sallberg M;
 XX WPI; 2002-055347/07.
 XX Novel peptide that binds to hepatitis B virus core or E antigen, useful
 XX for treating and preventing hepatitis B virus infection -
 XX Claim 2; Page 11; 82pp; English.
 XX The invention relates to an isolated or purified peptide (I) which binds
 XX Hepatitis B virus (HBV) core antigen (HBcAg) or HBV E antigen (HBeAg).
 XX (I) is useful for treating or preventing Hepatitis B virus (HBV)
 XX infection, by identifying a subject in need of a molecule that inhibits
 XX HBV infection, and providing the subject with (I). (I) is also useful
 XX for determining the presence of HBV in a biological sample, and for
 XX inhibiting B cell mediated processing and uptake of HBcAg and/or HBeAg,
 XX by determining whether (I) inhibits B cell mediated processing and
 XX uptake of HBcAg and/or HBeAg by performing an assay of T cell
 XX proliferation or cytokine production. (I) is also useful for modulating
 XX an immune system response. (I) is useful as a template for a design of
 XX synthetic molecules including peptides, derivatives or modified peptides,
 XX peptidomimetics and chemicals. (I) is also useful as biotechnological
 XX tool, diagnostic reagent and as active ingredient in pharmaceuticals.
 XX (I) is also useful as detection reagents in conventional
 XX immunohistochemical techniques, as diagnostic reagents to detect HBV in
 XX biological sample, and to determine the efficacy of an HBV treatment
 XX protocol by monitoring the levels of HBcAg and/or HBeAg during and after
 XX treatment. AAU70766-AAU70876 represent Hepatitis B virus (HBV) core
 XX antigen (HBcAg) or HBV E antigen (HBeAg) binding partners as described
 XX in the invention.
 XX Sequence 130 AA;
 SQ Query Match 88.0%; Score 44; DB 23; Length 130;
 Best Local Similarity 88.9%; Pred. No. 4.9;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RGTGTGFAY 9
 Db 97 RGKGTGFAY 105
 RESULT 14
 AAR04135
 ID AAR04135 standard; protein; 122 AA.
 AC AAR04135;
 XX 06-SEP-1990 (first entry)
 DT Anti-Leu 3a heavy chain variable region gene product, KOL/316 VH.
 DE HIV; AIDS; anti-Leu3A; vaccine; ds.
 KW Mus musculus.
 OS EP365209-A.
 PN 25-APR-1990.
 PD 11-OCT-1989; 89EP-0010415.
 PF 17-OCT-1988; 88US-0260558.
 PR (BECT) BECTON DICKINSON CO.
 XX Hinton R, Oi VT;
 XX WPI; 1990-126329/17.
 XX N-PSDB; AAQ04042.

Fri Feb 14 15:00:52 2003

XX New chimeric variants of murine antibody anti-leucine -
PT contg. human antibody regions, and DNA encoding sequences.
XX
XX Claim 5; Fig 5; 12pp; English.
XX
XX Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
CC used to form chimeric mouse-variable, human-constant region Abs
CC suggested as being useful as a vaccine to HIV.
XX
SQ Sequence 122 AA;

Query Match 80.0%; Score 40; DB 11; Length 122;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9
11111111:
103 RKGKTGFAY 111

RESULT 15
AAR04133
ID AAR04133 standard; protein; 136 AA.
XX
AC AAR04133;
XX
DT 06-SEP-1990 (first entry)
XX
DE Anti-Leu 3a heavy chain variable region gene product, 316 Vh.
XX
KW HIV; AIDS; anti-Leu3A; vaccine; ds.
XX
OS Mus musculus.
XX
PN EP365209-A.
XX
PD 25-APR-1990.
XX
PF 11-OCT-1989; 89EP-ON10415.
XX
PR 17-OCT-1988; 88US-0260558.
XX
PA (BECT) BECTON DICKINSON CO.
XX
PT Hinton R, Oi VT;

DR WPI; 1990-126329/17.
N-PSDB; AAQ04040.
XX
XX New chimeric variants of murine antibody anti-leucine -
PT contg. human antibody regions, and DNA encoding sequences.
XX
PS Claim 2; Fig 3; 12pp; English.
XX
XX Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
CC used to form chimeric mouse-variable, human-constant region Abs
CC suggested as being useful as a vaccine to HIV.
XX
SQ Sequence 136 AA;

Query Match 80.0%; Score 40; DB 11; Length 136;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9
11111111:
Db 117 RKGKTGFAY 125

Search completed: February 14, 2003, 11:15:43
Job time : 25.3871 secs

OTHER INFORMATION: Artificial Oligonucleotide
US-09-556-605-3

Query Match 88.0%; Score 44; DB 4; Length 130;

Best Local Similarity 88.9%; Pred. No. 1.8; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9

|| |||||

Db 97 RKGITGFAY 105

RESULT 3

US-09-130-491-15

Sequence 15, Application US/09130491

Patent No. 6416974

GENERAL INFORMATION:

APPLICANT: Holtzman, Douglas A.

APPLICANT: Goodearl, Andrew D.J.

TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-76, AND TANGO-83

FILE REFERENCE: 09404/041001

CURRENT APPLICATION NUMBER: US/09/130,491

CURRENT FILING DATE: 1998-08-07

EARLIER APPLICATION NUMBER: US 60/058,108

EARLIER FILING DATE: 1997-09-05

EARLIER APPLICATION NUMBER: US 60/054,961

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 15

LENGTH: 247

TYPE: PRT

ORGANISM: Homo sapiens

US-09-130-491-15

Query Match

Best Local Similarity 74.0%; Score 37; DB 4; Length 247;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGTGFAY 9

|||||

Db 205 GGTGTGFAY 212

RESULT 4

US-08-064-174-1

Sequence 1, Application US/08064174

Patent No. 5618540

GENERAL INFORMATION:

APPLICANT: QUENTIN-MILLET, Marie-Jose

APPLICANT: LISSOLO, Ling

TITLE OF INVENTION: SUBUNIT VACCINE FOR NEISSERIA

TITLE OF INVENTION: MENINGITIDIS INFECTIONS AND CORRESPONDING PURIFIED

TITLE OF INVENTION: SUBUNITS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: George Mason Bldg., Washington & Prince Sts.

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/064,174

FILING DATE: 25-MAY-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 91 12176

FILING DATE: 03-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Rea, Teresa Stanek

REGISTRATION NUMBER: 30,427

REFERENCE/DOCKET NUMBER: 016100-001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703/836-6620

TELEFAX: 703/836-2021

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 579 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-064-174-1

Query Match

Best Local Similarity 70.0%; Score 35; DB 1; Length 579;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9

|||||

Db 442 RGTGTGFAY 450

RESULT 5

US-08-066-167-1

Sequence 1, Application US/08066167

Patent No. 5618541

GENERAL INFORMATION:

APPLICANT: QUENTIN-MILLET, Marie-Jose

TITLE OF INVENTION: VACCINE AGAINST NEISSERIA MENINGITIDIS

TITLE OF INVENTION: INFECTIONS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: George Mason Bldg., Washington & Prince Sts.

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/066,167

FILING DATE: 02-JUN-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 91 12177

FILING DATE: 03-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Crane-Feury, Sharon E

REGISTRATION NUMBER: 36,113

REFERENCE/DOCKET NUMBER: 016100-002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 579 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Neisseria meningitidis 2394 subunit rbp2.

US-08-066-167-1

Query Match

Best Local Similarity 70.0%; Score 35; DB 1; Length 579;

Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9
||||| : |
Db 442 RGTGTWGY 450

RESULT 6
US-08-449-733-1
; Sequence 1, Application US/08449733
; Patent No. 5928650
; GENERAL INFORMATION:
; APPLICANT: QUENTIN-MILLET, Marie-Jose
; APPLICANT: LISSOLO, Ling
; TITLE OF INVENTION: SUBUNIT VACCINE FOR NEISSERIA
; TITLE OF INVENTION: MENINGITIDIS INFECTIONS AND CORRESPONDING PURIFIED
; TITLE OF INVENTION: SUBUNITS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,733
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 12176
; FILING DATE: 03-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,174
; FILING DATE: 25-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 016100-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703/836-6620
; TELEFAX: 703/836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-449-733-1
Query Match 70.0%; Score 35; DB 2; Length 579;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RGTGTGFAY 9
||||| : |
Db 442 RGTGTWGY 450
RESULT 7
US-08-671-978A-10
; Sequence 10, Application US/08671978A
; Patent No. 5959093
; GENERAL INFORMATION:
; APPLICANT: Saif, Linda J.
; APPLICANT: Parwani, Anil

; APPLICANT: Kim, Wonyong
; APPLICANT: Chang, Keong-OK
; TITLE OF INVENTION: ROTAVIRUS GENES
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CALFEE, HALTER & GRISWOLD
; STREET: 800 SUPERIOR AVENUE, SUITE 1400
; CITY: CLEVELAND
; STATE: OHIO
; COUNTRY: USA
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/671,978A
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLTRICK, MARY E
; REGISTRATION NUMBER: 34,829
; REFERENCE/DOCKET NUMBER: 22727/00133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 622-8200
; TELEFAX: (216) 241-0816
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 640 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-671-978A-10
Query Match 70.0%; Score 35; DB 2; Length 640;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 TGTGFAY 9
:|||||
Db 451 SGTGFAY 457
RESULT 8
US-09-314-242-10
; Sequence 10, Application US/09314242A
; Patent No. 6248575
; GENERAL INFORMATION:
; APPLICANT: Elizabeth J. Golightly
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
; FILE REFERENCE: 5556.200-US
; CURRENT APPLICATION NUMBER: US/09/314,242A
; EARLIER FILING DATE: 1999-05-18
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Trichoderma harzianum
US-09-314-242-10
Query Match 68.0%; Score 34; DB 4; Length 20;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RGTGTGFA 8
||| :|:

Db 3 RGTNTGYA 10

RESULT 9
US-08-933-750C-44
; Sequence 44, Application US/08933750C
; Patent No. 5932442
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,750C
; FILING DATE: September 23, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPINOT03
; CLONE: 2469611
US-08-933-750C-44

Query Match 68.0%; Score 34; DB 2; Length 251;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GTGTGFAY 9
Db 65 GPGTGFLY 72
RESULT 10
US-09-234-613-44
; Sequence 44, Application US/09234613
; Patent No. 6132973
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga

; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,613
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,750
; FILING DATE: September 23, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPINOT03
; CLONE: 2469611
US-09-234-613-44

Query Match 68.0%; Score 34; DB 4; Length 251;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTGTGFAY 9
Db 65 GPGTGFLY 72

RESULT 11
US-08-434-255-8
; Sequence 8, Application US/08434255
; Patent No. 5621089
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan P.
; APPLICANT: Outtrup, Helle
; APPLICANT: Dambmann, Claus
; APPLICANT: Aaslyng, Dorrit
; TITLE OF INVENTION: ALKALINE PROTEASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5621089o No. 5621089disk of No. 5621089th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:

us-09-701-001b-3.ra1

Fri Feb 14 15:00:52 2003

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/434,255
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Agis Dr., Cheryl H.
 ; REGISTRATION NUMBER: 34,086
 ; REFERENCE/DOCKET NUMBER: 3764.400-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 280 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-434-255-8

Query Match 68.0%; Score 34; DB 1; Length 280;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9
 Db 262 GTGTNFKY 269

RESULT 12
 ; Sequence 8, Application US/08459967
 ; Patent No. 5622841
 ; GENERAL INFORMATION:
 ; APPLICANT: Sloma, Alan P.
 ; APPLICANT: Outtrup, Helle
 ; APPLICANT: Dambmann, Claus
 ; APPLICANT: Aaslyng, Dorrit
 ; TITLE OF INVENTION: ALKALINE PROTEASE
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5622841 of No. 5622841 disk of No. 5622841th America, Inc.
 ; STREET: 405 Lexington Avenue, 64th Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/459,967
 ; FILING DATE: 02-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/434,255
 ; FILING DATE: 03-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Agis Dr., Cheryl H.
 ; REGISTRATION NUMBER: 34,086
 ; REFERENCE/DOCKET NUMBER: 3764.400-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 280 amino acids
 ; TYPE: amino acid

; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-459-967-8
 ; Query Match 68.0%; Score 34; DB 1; Length 280;
 ; Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 ; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9
 Db 262 GTGTNFKY 269

RESULT 13
 ; Sequence 8, Application US/08460327
 ; Patent No. 5622850
 ; GENERAL INFORMATION:
 ; APPLICANT: Sloma, Alan P.
 ; APPLICANT: Outtrup, Helle
 ; APPLICANT: Dambmann, Claus
 ; APPLICANT: Aaslyng, Dorrit
 ; TITLE OF INVENTION: ALKALINE PROTEASE
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5622850 of No. 5622850 disk of No. 5622850th America, Inc.
 ; STREET: 405 Lexington Avenue, 64th Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/460,327
 ; FILING DATE: 02-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/434,255
 ; FILING DATE: 03-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Agis Dr., Cheryl H.
 ; REGISTRATION NUMBER: 34,086
 ; REFERENCE/DOCKET NUMBER: 3764.400-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 280 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-460-327-8

Query Match 68.0%; Score 34; DB 1; Length 280;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9
 Db 262 GTGTNFKY 269

RESULT 14
 ; Sequence 8, Application US/08459871
 ; Patent No. 5650326
 ; GENERAL INFORMATION:
 ; APPLICANT: Sloma, Alan P.

APPLICANT: Outtrup, Helle
 APPLICANT: Dambmann, Claus
 APPLICANT: Aasiyang, Dorrit
 TITLE OF INVENTION: ALKALINE PROTEASE
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 56503260 No. 5650326disk of No. 5650326th America, Inc.
 STREET: 405 Lexington Avenue, 64th Floor
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,871
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/434,255
 FILING DATE: 03-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Agri Dr. Cheryl H.
 REGISTRATION NUMBER: 34,086
 REFERENCE/DOCKET NUMBER: 3764.400-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 280 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-459-871-8

Query Match 58.0%; Score 34; DB 1; Length 280;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9
 Db 262 GTGTNFKY 269

LT 15

9-024-532-2
 Sequence 2, Application US/09024532
 Patent No. 6245901
 GENERAL INFORMATION:
 APPLICANT: von der Osten, Claus
 APPLICANT: Olsen, Arne Agerlin
 APPLICANT: Roggen, Erwin Ludo
 TITLE OF INVENTION: A Modified Polypeptide
 FILE REFERENCE: 4923.204-US
 CURRENT APPLICATION NUMBER: US/09/024,532
 CURRENT FILING DATE: 1998-02-17
 EARLIER APPLICATION NUMBER: PCT/DK98/00046
 EARLIER FILING DATE: 1998-02-06
 EARLIER APPLICATION NUMBER: 0135/97
 EARLIER FILING DATE: 1997-02-06
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 280
 TYPE: PRT
 ORGANISM: bacillus sp.
 US-09-024-532-2
 Query Match 68.0%; Score 34; DB 4; Length 280;

Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 GTGTGFAY 9
 Db 262 GTGTNFKY 269
 Search completed: February 14, 2003, 11:20:48
 Job time : 9.12903 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:15:53 ; Search time 5.22581 Seconds
(without alignments)
44.001 Million cell updates/sec

Title: US-09-701-001B-3
Perfect score: 50
Sequence: 1 RGTGTGFAY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

140259 seqs, 2554876 residues
1 number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2.6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2.6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2.6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2.6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2.6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2.6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2.6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2.6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2.6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2.6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2.6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2.6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2.6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2.6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	44	88.0	20	10	US-09-839-447A-36
2	44	88.0	130	10	US-09-839-447A-3
3	37	74.0	247	12	US-10-105-929-15
4	37	74.0	248	9	US-09-759-130B-137
5	37	74.0	266	9	US-10-004-717-40
6	35	70.0	448	9	US-09-738-626-6795
7	35	70.0	576	10	US-09-925-297-787
8	34	68.0	251	9	US-09-992-598-6
9	34	68.0	251	9	US-09-989-293A-6
10	34	68.0	251	9	US-09-989-735-6
11	34	68.0	251	9	US-09-990-444-6
12	34	68.0	251	9	US-09-989-730-6
13	34	68.0	251	9	US-09-990-436-6
14	34	68.0	251	9	US-09-991-181-6
15	34	68.0	251	9	US-09-993-687-6
16	34	68.0	251	9	US-09-989-734-6
17	34	68.0	251	9	US-09-997-653-6
18	34	68.0	251	9	US-10-174-590-2
19	34	68.0	251	9	US-10-176-758-2

20	34	68.0	251	9	US-10-175-737-2	Sequence 2, Appli
21	34	68.0	251	9	US-09-993-667-6	Sequence 6, Appli
22	34	68.0	251	9	US-10-173-706-2	Sequence 2, Appli
23	34	68.0	251	9	US-10-175-738-2	Sequence 2, Appli
24	34	68.0	251	9	US-10-175-752-2	Sequence 2, Appli
25	34	68.0	251	9	US-10-176-482-2	Sequence 2, Appli
26	34	68.0	251	9	US-10-176-913-2	Sequence 2, Appli
27	34	68.0	251	9	US-10-176-913-2	Sequence 2, Appli
28	34	68.0	251	9	US-10-180-552-2	Sequence 2, Appli
29	34	68.0	251	9	US-10-180-557-2	Sequence 2, Appli
30	34	68.0	251	9	US-09-990-438-6	Sequence 6, Appli
31	34	68.0	251	9	US-09-990-562-6	Sequence 6, Appli
32	34	68.0	251	9	US-09-997-428-6	Sequence 6, Appli
33	34	68.0	251	9	US-09-997-666-6	Sequence 6, Appli
34	34	68.0	251	9	US-10-173-700-2	Sequence 2, Appli
35	34	68.0	251	9	US-10-174-572-2	Sequence 2, Appli
36	34	68.0	251	9	US-10-174-579-2	Sequence 2, Appli
37	34	68.0	251	9	US-10-174-582-2	Sequence 2, Appli
38	34	68.0	251	9	US-10-174-588-2	Sequence 2, Appli
39	34	68.0	251	9	US-10-175-739-2	Sequence 2, Appli
40	34	68.0	251	9	US-10-175-740-2	Sequence 2, Appli
41	34	68.0	251	9	US-10-175-743-2	Sequence 2, Appli
42	34	68.0	251	9	US-10-176-488-2	Sequence 2, Appli
43	34	68.0	251	9	US-10-176-492-2	Sequence 2, Appli
44	34	68.0	251	9	US-10-176-747-2	Sequence 2, Appli
45	34	68.0	251	9	US-10-176-750-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-839-447A-36
; Sequence 36, Application US/09839447A
; Patent No. US20020058247A1
; GENERAL INFORMATION:
; APPLICANT: Salberg, Matti
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
; FILE REFERENCE: TRIPEP.020CPI
; CURRENT APPLICATION NUMBER: US/09/839,447A
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/556605
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-09-839-447A-36

Query Match 88.0% Score 44; DB 10; Length 20;
Best Local Similarity 88.9%; Pred. No. 0.096;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9
|||
DB 7 RKGTFAY 15

RESULT 2
US-09-839-447A-3
; Sequence 3, Application US/09839447A
; Patent No. US20020058247A1
; GENERAL INFORMATION:
; APPLICANT: Salberg, Matti
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
; FILE REFERENCE: TRIPEP.020CPI
; CURRENT APPLICATION NUMBER: US/09/839,447A

; CURRENT FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 09/556605
 ; PRIOR FILING DATE: 2000-04-21
 ; NUMBER OF SEQ ID NOS: 111
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 130
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial Peptide
 US-09-839-447A-3

Query Match 88.0%; Score 44; DB 10; Length 130;
 Best Local Similarity 88.9%; Pred. No. 0.58;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGCTGTGAY 9
 DB 97 RGCTGTGAY 105

RESULT 3

US-10-105-929-15
 ; Sequence 15, Application US/10105929
 ; Patent No. US20020137142A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Holtzman, Douglas A.
 ; APPLICANT: Goodearl, Andrew D.J.
 ; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
 ; FILE REFERENCE: 09404/041001
 ; CURRENT APPLICATION NUMBER: US/10/105,929
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 15
 ; LENGTH: 247
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-105-929-15

Query Match 74.0%; Score 37; DB 12; Length 247;
 Best Local Similarity 87.5%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGTGAY 9
 DB 205 GTGTGTGAY 212

RESULT 4

US-09-759-130B-137
 ; Sequence 137, Application US/09759130B
 ; Publication No. US20030022279A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: McCarthy, Sean A.
 ; APPLICANT: Fraser, Christopher C.
 ; APPLICANT: Sharp, John D.
 ; APPLICANT: Barnes, Thomas S.
 ; APPLICANT: Kirst, Susan J.
 ; APPLICANT: Mackay, Charles R.
 ; APPLICANT: Myers, Paul S.
 ; APPLICANT: Leiby, Kevin R.
 ; APPLICANT: Wrighton, Nicolas
 ; APPLICANT: Goodearl, Andrew
 ; APPLICANT: Holtzman, Douglas A.

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
 ; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
 ; FILE REFERENCE: MPI00-5350NMIM
 ; CURRENT APPLICATION NUMBER: US/09/759,130B
 ; CURRENT FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: US 09/479,249
 ; PRIOR FILING DATE: 2000-01-07
 ; PRIOR APPLICATION NUMBER: US 09/559,497
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: US 09/578,063
 ; PRIOR FILING DATE: 2000-05-24
 ; PRIOR APPLICATION NUMBER: US 09/333,159
 ; PRIOR FILING DATE: 1999-06-14
 ; PRIOR APPLICATION NUMBER: US 09/596,194
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 09/342,364
 ; PRIOR FILING DATE: 1999-06-29
 ; PRIOR APPLICATION NUMBER: US 09/608,452
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/393,996
 ; PRIOR FILING DATE: 1999-09-10
 ; PRIOR APPLICATION NUMBER: US 09/602,871
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: US 09/420,707
 ; PRIOR FILING DATE: 1999-10-19
 ; NUMBER OF SEQ ID NOS: 460
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 137
 ; LENGTH: 248
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 US-09-759-130B-137

Query Match 74.0%; Score 37; DB 9; Length 248;
 Best Local Similarity 87.5%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGTGAY 9
 DB 205 GTGTGTGAY 212

RESULT 5

US-10-004-717-40
 ; Sequence 40, Application US/10004717
 ; Publication No. US20020192665A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZOGHBI, HUDA Y.
 ; APPLICANT: YANG, Qi
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN
 ; TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS
 ; FILE REFERENCE: P01899US4
 ; CURRENT APPLICATION NUMBER: US/10/004,717
 ; CURRENT FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: 09/585,645
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: 60/176,993
 ; PRIOR FILING DATE: 2000-01-19
 ; PRIOR APPLICATION NUMBER: 60/137,060
 ; PRIOR FILING DATE: 1999-06-01
 ; NUMBER OF SEQ ID NOS: 69
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 40
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Zebra Fish
 US-10-004-717-40

Query Match 74.0%; Score 37; DB 9; Length 266;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9
||||| :
Db 209 RGTGVGY 217

RESULT 6
US-09-738-626-6795
; Sequence 6795, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TAKEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patentin ver. 3.0
; SEQ ID NO 6795
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6795

Query Match 70.0%; Score 35; DB 9; Length 448;
Best Local Similarity 87.5%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFA 8
||||| :
Db 386 RGTGTGAA 393

RESULT 7
US-09-925-297-787
; Sequence 787, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 787
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-297-787

Query Match 70.0%; Score 35; DB 10; Length 576;
Best Local Similarity 66.7%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9
||||| :
Db 499 RGHGTGFCF 507

RESULT 8
US-09-992-598-6
; Sequence 6, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijav, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026

; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088028
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088029
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088030
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088033
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088326
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088167
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/088202
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/088212
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/088217
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/088655
 ; PRIOR FILING DATE: 1998-06-09
 ; PRIOR APPLICATION NUMBER: 60/088734
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088738
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088742
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088810
 ; PRIOR FILING DATE: 1998-06-10
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 ; PRIOR FILING DATE: 1998-06-10
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 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088858
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 ; PRIOR APPLICATION NUMBER: 60/088876
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 ; PRIOR FILING DATE: 1998-06-12
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 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089600
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089653
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089801
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089907
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089908
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089947
 ; PRIOR FILING DATE: 1998-06-19
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 ; PRIOR APPLICATION NUMBER: 60/089952
 ; PRIOR FILING DATE: 1998-06-19
 ; PRIOR APPLICATION NUMBER: 60/090246
 ; PRIOR FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: 60/090252
 ; PRIOR FILING DATE: 1998-06-22
 ; PRIOR APPLICATION NUMBER: 60/090254
 ; PRIOR FILING DATE: 1998-06-22
 ; PRIOR APPLICATION NUMBER: 60/090349
 ; PRIOR FILING DATE: 1998-06-23
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 ; PRIOR FILING DATE: 1998-06-23
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 ; PRIOR FILING DATE: 1998-06-24
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 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090444
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090445
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090472
 ; PRIOR FILING DATE: 1998-06-24
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 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090540
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 ; PRIOR FILING DATE: 1998-06-24
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 ; PRIOR APPLICATION NUMBER: 60/090694
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090695
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090696
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090862
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 ; PRIOR APPLICATION NUMBER: 60/091360
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091478
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091544
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 68.0%; Score 34; DB 9; Length 251;
 Best Local Similarity 75.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTGTGFAY 9

Db 65 GPGTGFY 72

RESULT 9

US-09-989-293A-6
 ; Sequence 6, Application US/09989293A
 ; Patent No. US2002017164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerlitsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Faoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC66
 ; CURRENT APPLICATION NUMBER: US/09/989, 293A
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/075945
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/087106
 ; PRIOR FILING DATE: 1998-05-28
 ; PRIOR APPLICATION NUMBER: 60/087607
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/087609
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/087759
 ; PRIOR FILING DATE: 1998-06-02
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; PRIOR FILING DATE: 1998-07-09

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Query Match 68.0%; Score 34; DB 9; Length 251;
 Best Local Similarity 75.0%; Pred. No. 53;
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 Db 65 GPGTGLFY 72

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 ; Publication No. US20020193299A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David

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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989,735
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Query Match 68.0%; Score 34; DB 9; Length 251;
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 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
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 ; APPLICANT: Ferrari, Napoleone
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS ENCODING THE SAME
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us-09-701-001b-3.rapb

Fri Feb 14 15:00:53 2003

; APPLICANT: ROY, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810

Query Match 68.0%; Score 34; DB 9; Length 251;
Best Local Similarity 75.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 GTGTGFAY 9
1 11111
65 GPGTGFEL 72

RESULT 12
US-09-989-730-6
; Sequence 6, Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
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; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
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; PRIOR FILING DATE: 1998-06-18
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
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; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: 60/090676
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; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
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; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
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; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 68.0%; Score 34; DB 9; Length 251;
Best Local Similarity 75.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9
Db 65 GPGTGFY 72

RESULT 13
US-09-990-436-6
; Sequence 6, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730P1C14
;; CURRENT APPLICATION NUMBER: US/09/990,436
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
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;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
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;; PRIOR APPLICATION NUMBER: 60/083322
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;; PRIOR FILING DATE: 1998-06-11
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;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089440
;; PRIOR FILING DATE: 1998-06-16
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;; PRIOR FILING DATE: 1998-07-01
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 68.0% Score 34; DB 9; Length 251;
Best Local Similarity 75.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9
| | | | |
Db 65 GPGTGFY 72

RESULT 14

US-09-991-181-6
; Sequence 6, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2/30PIC53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
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;; PRIOR FILING DATE: 1997-11-13
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;; PRIOR APPLICATION NUMBER: 60/089440

Fri Feb 14 15:00:53 2003

; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
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; PRIOR FILING DATE: 1998-06-19
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 68.0%; Score 34; DB 9; Length 251;
Best Local Similarity 75.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFPAY 9
| | | | |
Db 65 GPGTGFY 72

RESULT 15

US-09-993-687-6
; Sequence 6, Application US/09933687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavins, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C11
; CURRENT APPLICATION NUMBER: US/09/993,687
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770

;	PRIOR APPLICATION NUMBER: 60/089539
;	PRIOR FILING DATE: 1998-06-17
;	PRIOR APPLICATION NUMBER: 60/089598
;	PRIOR FILING DATE: 1998-06-17
;	PRIOR APPLICATION NUMBER: 60/089599
;	PRIOR FILING DATE: 1998-06-17
;	PRIOR APPLICATION NUMBER: 60/089600
;	PRIOR FILING DATE: 1998-06-17
;	PRIOR APPLICATION NUMBER: 60/089653
;	PRIOR FILING DATE: 1998-06-17
;	PRIOR APPLICATION NUMBER: 60/089801
;	PRIOR FILING DATE: 1998-06-18
;	PRIOR APPLICATION NUMBER: 60/089907
;	PRIOR FILING DATE: 1998-06-18
;	PRIOR APPLICATION NUMBER: 60/089908
;	PRIOR FILING DATE: 1998-06-18
;	PRIOR APPLICATION NUMBER: 60/089947
;	PRIOR FILING DATE: 1998-06-19
;	PRIOR APPLICATION NUMBER: 60/089944
;	PRIOR FILING DATE: 1998-06-19
;	PRIOR APPLICATION NUMBER: 60/089952
;	PRIOR FILING DATE: 1998-06-19
;	PRIOR APPLICATION NUMBER: 60/090246
;	PRIOR FILING DATE: 1998-06-22
;	PRIOR APPLICATION NUMBER: 60/090252
;	PRIOR FILING DATE: 1998-06-22
;	PRIOR APPLICATION NUMBER: 60/090254
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;	PRIOR APPLICATION NUMBER: 60/090349
;	PRIOR FILING DATE: 1998-06-23
;	PRIOR APPLICATION NUMBER: 60/090355
;	PRIOR FILING DATE: 1998-06-23
;	PRIOR APPLICATION NUMBER: 60/090429
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090431
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090435
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090444
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;	PRIOR APPLICATION NUMBER: 60/090472
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090535
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;	PRIOR APPLICATION NUMBER: 60/090540
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090542
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090557
;	PRIOR FILING DATE: 1998-06-24
;	PRIOR APPLICATION NUMBER: 60/090676
;	PRIOR FILING DATE: 1998-06-25
;	PRIOR APPLICATION NUMBER: 60/090678
;	PRIOR FILING DATE: 1998-06-25
;	PRIOR APPLICATION NUMBER: 60/090690
;	PRIOR FILING DATE: 1998-06-25
;	PRIOR APPLICATION NUMBER: 60/090694
;	PRIOR FILING DATE: 1998-06-25
;	PRIOR APPLICATION NUMBER: 60/090695
;	PRIOR FILING DATE: 1998-06-25
;	PRIOR APPLICATION NUMBER: 60/090696
;	PRIOR FILING DATE: 1998-06-25
;	PRIOR APPLICATION NUMBER: 60/090862
;	PRIOR FILING DATE: 1998-06-26
;	PRIOR APPLICATION NUMBER: 60/090863
;	PRIOR FILING DATE: 1998-06-26
;	PRIOR APPLICATION NUMBER: 60/091360
;	PRIOR FILING DATE: 1998-07-01
;	PRIOR APPLICATION NUMBER: 60/091478
;	PRIOR FILING DATE: 1998-07-02
;	PRIOR APPLICATION NUMBER: 60/091544

; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 68.0%; Score 34; DB 9; Length 251;
 Best Local Similarity 75.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 GTGTGFAY 9
 | | | | |
 65 GPGTGFLY 72

Search completed: February 14, 2003, 11:21:30
 Job time : 6.22581 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:12:02 ; Search time 9 Seconds
(without alignments)
96.134 Million cell updates/sec

Title: US-09-701-001B-3
Perfect score: 50
Sequence: 1 RGTGTGFAY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	78.0	685	2 A83499	probable lipoxigen
2	38	76.0	483	2 E84976	tlld protein [impo
3	38	76.0	568	2 A45804	Ig mu chain C regi
4	37	74.0	280	2 A39484	androgen-withdraw
5	37	74.0	502	2 AE2040	hypothetical prote
6	36	72.0	101	2 T10856	carboxypeptidase C
7	36	72.0	149	2 S19130	rab15 protein - wh
8	36	72.0	163	2 S01152	RAB21 protein - ri
9	36	72.0	165	2 T03392	probable dehydrin
10	36	72.0	411	1 A35275	carboxypeptidase C
11	36	72.0	423	1 A33383	probable MFS trans
12	36	72.0	429	1 T03607	probable carboxype
13	36	72.0	498	1 A29412	carboxypeptidase C
14	36	72.0	500	1 S22330	carboxypeptidase C
15	36	72.0	1077	2 H96007	probable acriflavi
16	36	72.0	3295	2 AE0074	probable adhesin Y
17	35	70.0	163	2 A89904	conserved hypothet
18	35	70.0	398	2 C95278	hypothetical prote
19	35	70.0	401	2 AD2451	serine proteinase
20	35	70.0	429	2 AD1894	serine proteinase
21	35	70.0	452	2 S77538	TXBP151 - human
22	35	70.0	563	2 G02043	period clock prote
23	35	70.0	713	1 UMMS	outer layer protei
24	35	70.0	736	1 VPXRPC	outer capsid spike
25	35	70.0	744	2 S45060	outer capsid spike
26	35	70.0	744	2 S45061	villin - chicken
27	35	70.0	826	1 A31822	Ig heavy chain - c
28	35	70.0	1005	2 T18537	hypothetical prote
29	34	68.0	99	2 F82709	

ALIGNMENTS

RESULT 1

A83499

Probable lipoxigenase Pali69 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: A83499
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
Nature 406, 959-964, 2000
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A83499
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-685 <STO>
A:Cross-references: GB:AE004547; GB:AE004091; MID:g9947089; PIDN:AAG04558.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: Pali69

Query Match 78.0%; Score 39; DB 2; Length 685;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9
| | | | |
Db 305 TGTGFAY 311

RESULT 2

E84976

tlld protein [imported] - Buchnera sp. (strain APS)

C:Species: Buchnera sp.

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: E84976

R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp

A:Reference number: A84930; MUID:20445173; PMID:10993077

A:Accession: E84976

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-483 <STO>

A:Cross-references: GB:AF000398; GSPDB:GN00144

A:Experimental source: strain APS

C:Genetics:

A:Gene: tlld; BU398

C:Superfamily: Escherichia coli tlld protein

Query Match 76.0%; Score 38; DB 2; Length 483;
Best Local Similarity 77.8%; Pred. No. 49;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RCTGTGFAY 9
||| |||||
Db 72 RGTGTGFAY 80

RESULT 3

A45804
Ig mu chain C region precursor, secreted form - channel catfish
C:Species: Ictalurus punctatus (channel catfish)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
C:Accession: A45804; A30331; S12833
R:Ghafari, S.H.; Lobb, C.J.
J. Immunol. 143, 2730-2739, 1989
A:Title: Nucleotide sequence of channel catfish heavy chain cDNA and genomic blot analysis
A:Reference number: A45804; MUID:90010149; PMID:2507636
A:Accession: A45804
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-568 <GHA>
A:Cross-references: GB:M27230; NID:g213318; PIDN:AAA79003.1; PID:g213319
J. Affari, S.H.; Lobb, C.J.
J. Immunol. 142, 1356-1365, 1989
A:Title: Cloning and sequence analysis of channel catfish heavy chain cDNA indicate phylogenetic relationship with the channel catfish heavy chain cDNA
A:Reference number: A30331; MUID:89124381; PMID:2492581
A:Accession: A30331
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 325-568 <GH2>
A:Cross-references: GB:M23733; NID:g213316; PIDN:AAA49329.1; PID:g213317
R:Wilson, M.R.; Marcuz, A.; van Ginkel, F.; Miller, N.W.; Clem, L.W.; Middleton, D.; War
Nucleic Acids Res. 18, 5227-5233, 1990
A:Title: The immunoglobulin M heavy chain constant region gene of the channel catfish, Ictalurus punctatus (Pomoxys ananistatus) (Pomoxys ananistatus)
A:Reference number: S12833; MUID:90384824; PMID:2119496
A:Accession: S12833
A:Molecule type: DNA
A:Residues: 135-568 <WIL>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; heterotetramer; immunoglobulin
F:1-17/Domain: signal sequence #status Predicted <SIG>
F:18-568/Product: Ig mu chain C region, secreted form #status Predicted <MAT>
F:31-113/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 38; DB 2; Length 568;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTGTGFA 8
|||||
70 GTGTGFA 76

RESULT 4

A39484
androgen-withdrawal apoptosis protein RVP1, prostatic - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 04-Mar-2000
C:Accession: A39484
R:Briehl, M.M.; Miesfeld, R.L.
Mol. Endocrinol. 5, 1381-1388, 1991
A:Title: Isolation and characterization of transcripts induced by androgen withdrawal and androgen withdrawal apoptosis protein RVP1
A:Reference number: A39484; MUID:92130987; PMID:1723140
A:Accession: A39484
A:Molecule type: mRNA
A:Residues: 1-280 <BRI>
A:Cross-references: GB:M74067; NID:g205857; PIDN:AAA41760.1; PID:g205858
C:Genetics:
C:Superfamily: rat androgen-withdrawal apoptosis protein RVP1

Query Match 74.0%; Score 37; DB 2; Length 280;
Best Local Similarity 87.5%; Pred. No. 43;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9
|||||
Db 205 GTGTGFAY 212

RESULT 5

AE2040
hypothetical protein all1875 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AE2040
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Nostoc sp. strain PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2040
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-502 <KOR>
A:Cross-references: GB:BA000019; PIDN:BA073574.1; PID:g17130965; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1875

Query Match 74.0%; Score 37; DB 2; Length 502;
Best Local Similarity 77.8%; Pred. No. 75;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9
||| |||||
Db 159 RGTGTGFAY 167

RESULT 6

TI0856
carboxypeptidase C (EC 3.4.16.5) - mung bean (fragment)
N:Alternate names: serine carboxypeptidase II
C:Species: Vigna radiata (mung bean)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 08-Dec-2000
C:Accession: TI0856
R:Lee, K.; Tan-Wilson, A.L.; Wilson, K.A.
Submitted to the EMBL Data Library, February 1996
A:Reference number: Z17185
A:Accession: TI0856
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-101 <LEE>
A:Cross-references: EMBL:U49382; NID:g1223915; PID:g1223916
A:Experimental source: strain Jumbo; tissue_type cotyledons; clone pKL054
C:Keywords: hydrolase; serine carboxypeptidase

Query Match 72.0%; Score 36; DB 2; Length 101;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9
|||||
Db 49 TGTGFAY 55

RESULT 7

S19130
rab15 protein - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Aug-1999
C:Accession: S19130; S16758
R:King, S.W.; Joshi, C.P.; Nguyen, H.T.
Plant Mol. Biol. 18, 119-121, 1992

A:Title: DNA sequence of an ABA-responsive gene (rab 15) from water-stressed wheat roots

A:Reference number: S19130; MUID:92119217; PMID:1531029
A:Accession: S19130
A:Molecule type: mRNA
A:Residues: 1-149 <KIN>
A:Cross-references: EMBL:X59133; NID:g21850; PIDN:CAA41850.1; PID:g21851
C:Genetics:
A:Gene: rab15
C:Superfamily: dehydrin-like protein

Query Match 72.0%; Score 36; DB 2; Length 149;
Best Local Similarity 87.5%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTGTGFAY 9
|||||
Db 99 GTGTGGAY 106

RESULT 8

S01152
RAB21 protein - rice
C:Species: Oryza sativa (rice)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1990 #text_change 20-Aug-1999
C:Accession: S01152
R:Mundy, J.; Chua, N.H.
EMBO J. 7, 2279-2286, 1988
A:Title: Abscisic acid and water-stress induce the expression of a novel rice gene.
A:Reference number: S01152; MUID:89052639; PMID:2973410
A:Accession: S01152
A:Molecule type: DNA
A:Residues: 1-163 <MUN>
A:Cross-references: EMBL:X00842; NID:g20316; PIDN:CAA68765.1; PID:g295826
A:Note: the authors translated the codon GCG for residue 28 as Gly
C:Genetics:
A:Gene: RAB21
A:Introns: 70/3
C:Superfamily: dehydrin-like protein
C:Keywords: seed

Query Match 72.0%; Score 36; DB 2; Length 163;
Best Local Similarity 87.5%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTGTGFAY 9
|||||
114 GTGTGGAY 121

RESULT 9

T03392
probable dehydrin - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Aug-1999
C:Accession: T03392
R:McEvoy, S.M.; Sheoran, I.S.; Saini, H.S.
submitted to the EMBL Data Library, June 1996
A:Description: A rice cDNA encoding a late embryogenesis abundant protein.
A:Reference number: Z14923
A:Accession: T03392
A:Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1-165 <MCE>
A:Cross-references: EMBL:U60097; NID:g1399912; PIDN:AAB03330.1; PID:g1399913
C:Superfamily: dehydrin-like protein

Query Match 72.0%; Score 36; DB 2; Length 165;
Best Local Similarity 87.5%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTGTGFAY 9
|||||
Db 116 GTGTGGAY 123

RESULT 10

A35275
carboxypeptidase C (EC 3.4.16.5) - barley
N:Alternate names: carboxypeptidase III
C:Species: Hordeum vulgare (barley)
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
C:Accession: A35275
R:Sorensen, S.B.; Svendsen, I.; Breddam, K.
Carlsberg Res. Commun. 54, 193-202, 1989
A:Title: Primary structure of carboxypeptidase III from malted barley.
A:Reference number: A35275; MUID:90315015; PMID:2639682
A:Accession: A35275
A:Molecule type: protein
A:Residues: 1-411 <SOR>
A:Note: 185-Val was also found
C:Superfamily: serine carboxypeptidase
C:Keywords: blocked.amino end; glycoprotein; hydrolase; serine carboxypeptidase
F:1/Modified site: blocked.amino end (Leu) (probably acetylated) #status experimental
F:71/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:143,331,388/Active site: Ser, Asp, His #status predicted

Query Match 72.0%; Score 36; DB 1; Length 411;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGTGFAY 9
|||||
Db 94 TGTGFSY 100

RESULT 11

A83383
probable MFS transporter PA2114 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: A83383
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A83383
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-423 <STO>
A:Cross-references: GB:AE004638; GB:AE004091; NID:g9948116; PIDN:AAG05502.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2114
C:Superfamily: Escherichia coli hypothetical protein b4279

Query Match 72.0%; Score 36; DB 2; Length 423;
Best Local Similarity 66.7%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RGTGTGFAY 9
|||||
Db 360 RGSQGFY 368

RESULT 12

T03607
probable carboxypeptidase C (EC 3.4.16.5) cbp31 - rice
N:Alternate names: serine-type carboxypeptidase homolog
C:Species: Oryza sativa (rice)
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 21-Jul-2000
C:Accession: T03607
R:Washio, K.; Ishikawa, K.
Plant Physiol. 105, 1275-1280, 1994
A:Title: Organ-specific and hormone-dependent expression of genes for serine carboxypeptidase

A:Reference number: 214975; MUID:95062718; PMID:7972496

A:Accession: T03607

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-429 <WAS>

A:Cross-references: EMBL:DL7587; NID:g409581; PIDN:BA04511.1; PID:g409582

A:Experimental source: cv. Yukihikari

C:Genetics:

A:Gene: cbp31

C:Superfamily: serine carboxypeptidase

C:Keywords: glycoprotein; hydrolase; serine carboxypeptidase

F:76,414,417/Binding site: carboxylate (Asn) (covalent) #status predicted

F:148,336,393/Active site: Ser, Asp, His #status predicted

Query Match

Best Local Similarity 72.0%; Score 36; DB 1; Length 429;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGTGFAY 9

|||||:|

99 TGTGFSY 105

RESULT 13

A29412

carboxypeptidase C (EC 3.4.16.5) precursor - wheat

N:Alternate names: carboxypeptidase Y homolog

C:Species: Triticum aestivum (common wheat)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Nov-1999

C:Accession: A29412

R:Baulcombe, D.C.; Barker, R.F.; Jarvis, M.G.

J. Biol. Chem. 262, 13726-13735, 1987

A:Title: A gibberellin responsive wheat gene has homology to yeast carboxypeptidase Y.

A:Reference number: A29412; MUID:88007602; PMID:2820978

A:Accession: A29412

A:Molecule type: mRNA

A:Residues: 1-499 <BAU>

C:Genetics:

A:Introns: 100/2; 156/3; 196/3; 244/3; 295/1; 324/3; 411/1; 455/3

C:Superfamily: serine carboxypeptidase

C:Keywords: glycoprotein; hydrolase; serine carboxypeptidase; zymogen

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-73/Domain: propeptide #status predicted <PRO>

F:74-484/Product: carboxypeptidase C #status predicted <MAT>

F:485-499/Domain: carboxyl-terminal propeptide #status predicted <CPRO>

F:144/Binding site: carboxylate (Asn) (covalent) #status predicted

F:216,404,461/Active site: Ser, Asp, His #status predicted

Query Match

Best Local Similarity 72.0%; Score 36; DB 1; Length 499;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGTGFAY 9

|||||:|

Db 167 TGTGFSY 173

RESULT 14

S22530

carboxypeptidase C (EC 3.4.16.5) precursor - rice

N:Alternate names: carboxypeptidase III

C:Species: Oryza sativa (rice)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Nov-1999

C:Accession: S22530

R:Washio, K.; Ishikawa, K.

Plant Mol. Biol. 19, 631-640, 1992

A:Title: Structure and expression during the germination of rice seeds of the gene for a

A:Reference number: S22530; MUID:9329723; PMID:1627776

A:Accession: S22530

A:Molecule type: DNA

A:Residues: 1-500 <WAS>

A:Cross-references: EMBL:S40458

C:Genetics:

A:Introns: 100/2; 156/3; 196/3; 244/3; 295/1; 324/3; 411/1; 455/3

C:Superfamily: serine carboxypeptidase

C:Keywords: glycoprotein; hydrolase; serine carboxypeptidase; zymogen

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-73/Domain: propeptide #status predicted <PRO>

F:74-484/Product: carboxypeptidase C #status predicted <MAT>

F:485-499/Domain: carboxyl-terminal propeptide #status predicted <CPRO>

F:144/Binding site: carboxylate (Asn) (covalent) #status predicted

F:216,404,461/Active site: Ser, Asp, His #status predicted

Query Match

Best Local Similarity 72.0%; Score 36; DB 1; Length 500;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGTGFAY 9

|||||:|

Db 167 TGTGFSY 173

RESULT 15

H96007

probable acriflavin resistance protein [imported] - Sinorhizobium meliloti (strain 10

C:Species: Sinorhizobium meliloti

C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C:Accession: H96007

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her

proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A:Title: The complete sequence of the 1,883-Kb pSymb megaplasmid from the N2-fixing e

A:Reference number: A95842; MUID:21396508; PMID:11481431

A:Accession: H96007

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1077 <KUR>

A:Cross-references: GB:AL591985; PIDN:CAC49728.1; PID:gl5141215; GSPDB:GN00167

A:Experimental source: strain 1021, megaplasmid pSymb

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau

heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wellis, D.H.; Wong, K.; Yeh,

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: acrF: SMB21498

A:Genome: plasmid

C:Superfamily: acriflavin resistance protein

Query Match

Best Local Similarity 72.0%; Score 36; DB 2; Length 1077;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTGTGFAY 9

|||||:|

Db 673 GTGGGFAY 680

Search completed: February 14, 2003, 11:19:46

Job time : 11 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:05:27 ; Search time 4.64516 Seconds
(without alignments)
80.360 Million cell updates/sec

Title: US-09-701-001b-3
Perfect score: 50
Sequence: 1 RGTGTGFAY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Hit: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	76.0	483	1 TLDD_BUCAI	P57478 buchnera ap
2	37	74.0	219	1 CLD3_MOUSE	Q92099 mus musculus
3	37	74.0	219	1 CLD3_RAT	Q03400 rattus norv
4	36	72.0	149	1 DH15_WHEAT	Q00742 triticum ae
5	36	72.0	163	1 DH21_ORYSA	P12253 oryza sativ
6	36	72.0	429	1 CBPX_ORYSA	P52712 oryza sativ
7	36	72.0	500	1 CBP3_ORYSA	P37891 oryza sativ
8	36	72.0	500	1 CBP3_WHEAT	P11515 triticum ae
9	36	72.0	508	1 CBP3_HORVU	P21529 hordeum vul
10	35	70.0	672	1 PHX5_MOUSE	P08399 mus musculus
11	35	70.0	736	1 VP4_ROTPE	P26193 porcine rot
12	35	70.0	826	1 VILI_CHICK	P02640 gallus gall
13	34	68.0	111	1 CYC_CHLRE	P15451 chlanydomon
14	34	68.0	233	1 YOD2_CAEEL	P34594 caenorhabdi
15	34	68.0	281	1 CCAS_CHICK	Q42398 gallus gall
16	34	68.0	291	1 SUHB_MYCLE	P46813 mycobacteri
17	34	68.0	369	1 H181_STRCO	P16246 streptomyce
18	34	68.0	375	1 Y4ED_RHISN	P55427 rhizobium s
19	34	68.0	450	1 TBA2_HUMAN	Q13748 homo sapien
20	34	68.0	450	1 TBA3_MOUSE	P05214 mus musculus
21	34	68.0	450	1 TBA2_ONCMY	P18288 oncorhynch
22	34	68.0	451	1 TBA2_HOMAM	Q94570 homarus ame
23	34	68.0	477	1 GLGA_STRPN	Q97qs5 streptococ
24	34	68.0	640	1 Y0AA_HAEIN	P44680 haemophilus
25	34	68.0	905	1 CTPE_MYCTU	Q10860 mycobacteri
26	34	68.0	1394	1 HAP_HAEIN	P45387 haemophilus
27	34	68.0	1401	1 RPOC_VIBCH	Q9kv29 vibrio chol
28	34	68.0	1415	1 RPOC_HAEIN	P43739 haemophilus
29	33	66.0	157	1 Y188_RICPR	Q67dx6 rickettsia
30	33	66.0	356	1 PROB_AQUAE	O67209 aquifex aeo
31	33	66.0	385	1 ARGD_BACSU	P36839 bacillus su
32	33	66.0	405	1 YJHB_ECOLI	P39352 escherichia
33	33	66.0	445	1 ALCP_BACP3	P30145 bacillus ps

34	33	66.0	561	1 HEMA_IACKG	P12581 influenza a
35	33	66.0	637	1 DXS_NEIMA	Q9jw13 neisseria m
36	33	66.0	637	1 DXS_NEIMB	Q9jxv7 neisseria m
37	33	66.0	887	1 SM6B_RAT	O70141 rattus norv
38	33	66.0	893	1 DSCI_BOVIN	Q01107 bos taurus
39	33	66.0	984	1 KBFI_CHICK	Q04861 gallus gall
40	32	64.0	204	1 RL15_ORCLI	Q9xyc2 orconectes
41	32	64.0	309	1 ALSK_ECOLI	P32718 escherichia
42	32	64.0	321	1 HHOA_ARATH	Q9sel7 arabidopsis
43	32	64.0	338	1 GALE_PASHA	O59678 pasteurella
44	32	64.0	339	1 GALE_BACSU	P55180 bacillus su
45	32	64.0	347	1 GALE_RAT	P18645 rattus norv

ALIGNMENTS

RESULT 1
TLDD_BUCAI STANDARD; PRT; 483 AA.
AC P57478;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE TLDD protein homolog.
GN TLDD OR BU398.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum)
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo. 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- SIMILARITY: BELONGS TO THE TLDD/PMBA FAMILY.
CC
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CC
CC EMBL; AP001119; BABI3101.1; -
DR InterPro; IPR002510; PmbA_TLDD.
DR Pfam; PF01523; PmbA_TLDD; 1.
KW Complete proteome.
SQ SEQUENCE 483 AA; 52977 MW; A05CE98518720EBA CRC64;

Query Match 76.0%; Score 38; DB 1; Length 483;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9
|||
Db 72 RGTGTGFAY 80

RESULT 2
CLD3_MOUSE STANDARD; PRT; 219 AA.
ID CLD3_MOUSE
AC Q920G9; Q91X40;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Claudin-3 (Clostridium perfringens enterotoxin receptor 2) (CPE-
GN receptor 2) (CPE-R 2).
CLDN3 OR CPETR2.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=99097345; PubMed=9878248;
 RA Paperna T., Peoples R., Wang Y.K., Kaplan P., Francke U.;
 RT "Genes for the CPE receptor (CPETR1) and the human homolog of RVPL
 RT (CPETR2) are localized within the Williams-Beuren syndrome deletion.";
 RL Genomics 54:453-459(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=99110921; PubMed=9892664;
 RA Morita K., Furuse M., Fujimoto K., Tsukita S.;
 RT "Claudin multigene family encoding four-transmembrane domain protein
 RT components of tight junction strands.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:511-516(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX TISSUE=Colon;
 RA Strausberg R.;
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
 CC produced by alternative splicing.
 CC -!- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF095905; AAD14608.1; -;
 DR EMBL; AF087821; AAD09756.1; -;
 DR EMBL; BC012650; AAH12650.1; -;
 DR MGI; MGI:1329044; Clgdn3.
 DR InterPro; IPR001832; Claudin.
 DR Pfam; PF00822; PMP22_Claudin; 1.
 DR PRINTS; PR01077; CLAUDIN.
 DR PROSITE; PS01346; CLAUDIN; 1.
 DR TIGHT junction; Transmembrane; Alternative splicing.
 FT TRANSMEM 9 29 POTENTIAL.
 FT TRANSMEM 81 101 POTENTIAL.
 FT TRANSMEM 116 136 POTENTIAL.
 FT TRANSMEM 160 180 POTENTIAL.
 FT VARSPLIC 72 91 MISSING (IN ISOFORM 2).
 FT SEQUENCE 219 AA; 23284 MW; 62F67810D9B9BD37 CRC64;
 SQ
 Query Match 74.0%; Score 37; DB 1; Length 219;
 Best Local Similarity 87.5%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GTGTGFAY 9
 |||||
 Db 206 GTGTGTAY 213
 RESULT 3
 CLD3_RAT
 ID CLD3_RAT STANDARD; PRT; 219 AA.
 AC Q63400;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Claudin-3 (Ventral prostate.1 protein) (RVPL).
 GN CLDN3.
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92130987; PubMed=1723140;
 RA Brighl M.M., Miesfeld R.L.;
 RT "Isolation and characterization of transcripts induced by androgen
 RT withdrawal and apoptotic cell death in the rat ventral prostate.";
 RL Mol. Endocrinol. 5:1381-1388(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Keen T.J., Inglehearn C.F.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; M74067; AAA41760.1; -;
 DR EMBL; AJ011656; CAA09727.1; -;
 DR InterPro; IPR001832; Claudin.
 DR Pfam; PF00822; PMP22_Claudin; 1.
 DR PRINTS; PR01077; CLAUDIN.
 DR PROSITE; PS01346; CLAUDIN; 1.
 DR TIGHT junction; Transmembrane.
 FT TRANSMEM 9 29 POTENTIAL.
 FT TRANSMEM 81 101 POTENTIAL.
 FT TRANSMEM 116 136 POTENTIAL.
 FT TRANSMEM 162 182 POTENTIAL.
 FT CONFLICT 4 4 G -> S (IN REF. 1).
 FT CONFLICT 55 55 MISSING (IN REF. 1).
 FT CONFLICT 217 219 DIV -> YTSRPGARTPHHHYQPSMYTPRACSLASETT
 PPSRRLQTPRSLLARLEEDRQGVFPSPVAT (IN REF. 1).
 FT SEQUENCE 219 AA; 23314 MW; 820CC6BFC20D122D CRC64;
 SQ
 Query Match 74.0%; Score 37; DB 1; Length 219;
 Best Local Similarity 87.5%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GTGTGFAY 9
 |||||
 Db 206 GTGTGTAY 213
 RESULT 4
 DH15_WHEAT
 ID DH15_WHEAT STANDARD; PRT; 149 AA.
 AC Q00742;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE Dehydrin RAB 15.
 GN RAB 15.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. TAM W-101; TISSUE=Root;
 RX MEDLINE=92119217; PubMed=1531029;
 RA King S.W., Joshi C.P., Nguyen H.T.;

"DNA sequence of an ABA-responsive gene (rab 15) from water-stressed wheat roots.";
 Plant Mol. Biol. 18:119-121(1992).
 CC -!- INDUCTION: BY ABSICISIC ACID AND WATER STRESS.
 CC -!- SIMILARITY: BELONGS TO THE PLANT DEHYDRIN FAMILY.
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 CC
 DR EMBL; X59133; CAA41850.1; -.
 DR PIR; S16758; S16758.
 DR PIR; S19130; S19130.
 DR InterPro; IPR000167; Dehydrin.
 Pfam; PF00257; dehydrin; 1.
 PROSITE; PS00315; DEHYDRIN_1; 1.
 PROSITE; PS00823; DEHYDRIN_2; 2.
 KW Dehydrin.
 FT DOMAIN 55 64 POLY-SER.
 SQ SEQUENCE 149 AA; 15766 MW; 72183F7A99E467B1 CRC64;
 Query Match 72.0%; Score 36; DB 1; Length 149;
 Best Local Similarity 87.5%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GTGTGFAY 9
 DB 99 GTGTGGAY 106
 RESULT 5
 ID DH21-ORYSA STANDARD; PRT; 163 AA.
 AC P12253;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Water-stress inducible protein RAB21.
 GN RAB21.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxID=4530;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=cv. Indica-IR36; TISSUE=Seed;
 RX MEDLINE=89052639; PubMed=2973410;
 RA Mundy J.W., Chua N.-H.;
 RT "Abscisic acid and water-stress induce the expression of a novel rice gene.";
 RL EMBO J. 7:2279-2286(1988).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- INDUCTION: BY ABSICISIC ACID (ABA) AND WATER STRESS.
 CC -!- SIMILARITY: BELONGS TO THE PLANT DEHYDRIN FAMILY.
 CC
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 CC
 DR EMBL; Y00842; CAA68765.1; -.
 DR PIR; S01152; S01152.
 DR InterPro; IPR000167; Dehydrin.
 Pfam; PF00257; dehydrin; 1.
 PROSITE; PS00315; DEHYDRIN_1; 1.

DR PROSITE; PS00823; DEHYDRIN_2; 2.
 KW Dehydrin; Seed: Seed embryo; Repeat.
 FT DOMAIN 63 71 TYPE A.
 FT REPEAT 3 28 TYPE B.
 FT REPEAT 79 96 TYPE A.
 FT REPEAT 114 140 TYPE B.
 FT REPEAT 147 163 TYPE B.
 SQ SEQUENCE 163 AA; 16543 MW; 47FEDAD256DE7ACF CRC64;
 Query Match 72.0%; Score 36; DB 1; Length 163;
 Best Local Similarity 87.5%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GTGTGFAY 9
 DB 114 GTGTGGAY 121
 RESULT 6
 ID CBPX-ORYSA STANDARD; PRT; 429 AA.
 AC P52712;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Serine carboxypeptidase-like precursor (EC 3.4.16.-).
 GN CBP31.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxID=4530;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=cv. Yukihikari;
 RA Washio K., Ishikawa K.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Release of a C-terminal amino acid with a broad specificity.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.
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 CC
 DR EMBL; D17587; BAA04511.1; -.
 DR HSSP; P00729; LYSC.
 DR MEROPS; S10.009; -.
 DR InterPro; IPR000379; Ser_estrs_site.
 DR InterPro; IPR001563; Serine_carbpept.
 Pfam; PF00450; serine_carbpept; 1.
 PRINTS; PR00724; CRBOXYPTASEC.
 DR ProDom; PD001189; Serine_carbpept; 1.
 DR PROSITE; PS00131; CARBOXYPEPT_SER_SER; 1.
 DR PROSITE; PS00560; CARBOXYPEPT_SER_HIS; 1.
 KW Hydrolase; Carboxypeptidase; Glycoprotein; Signal.
 FT SIGNAL 1 ? POTENTIAL.
 FT CHAIN ? 429 SERINE CARBOXYPEPTIDASE-LIKE.
 FT ACT_SITE 148 148 BY SIMILARITY.
 FT ACT_SITE 336 336 BY SIMILARITY.
 FT ACT_SITE 393 393 BY SIMILARITY.
 FT BINDING 339 339 SUBSTRATE (BY SIMILARITY).
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 429 AA; 47746 MW; 1D5A668544325BBI CRC64;
 Query Match 72.0%; Score 36; DB 1; Length 429;
 Best Local Similarity 85.7%; Pred. No. 48;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9
|||||:|

Db 99 TGTGFSY 105

RESULT 7
CBP3_ORYSA
ID CBP3_ORYSA STANDARD; PRT; 500 AA.
AC P37891;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine carboxypeptidase III precursor (EC 3.4.16.5).
GN CBP3.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
[1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Yukihikari; TISSUE=Seed;
RX MEDLINE=92329723; PubMed=1627776;
RA Washio K., Ishikawa K.;
RT "Structure and expression during the germination of rice seeds of the
RT gene for a carboxypeptidase.";
RL Plant Mol. Biol. 19:631-640(1992).
CC -!- CATALYTIC ACTIVITY: Release of a C-terminal amino acid with a
CC broad specificity.
CC -!- SUBUNIT: MONOMER (PROBABLE).
CC -!- INDUCTION: BY GIBBERELIC ACID (GA). INHIBITED BY ABSCISIC ACID
CC (ABA).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.
CC
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CC
CC EMBL: D10985; BAA01757.1; -.
CC PIR: S22530; S22530.
CC HSSP: P00729; LYSC.
CC MEROPS: S10.009; -.
CC InterPro: IPR000379; Ser_estrs.site.
CC ProDom: PD001189; Serine_carbpept. 1.
CC PROSITE: PS00131; CARBOXYPEPT_SER_SER; 1.
CC PROSITE: PS00560; CARBOXYPEPT_SER_HIS; 1.
CC Pfam: PF00450; serine_carbpept; 1.
CC PRINTS: PR00724; CRBOXYPTASEC.
CC ProDom: PD001189; Serine_carbpept; 1.
CC PROSITE: PS00131; CARBOXYPEPT_SER_SER; 1.
CC PROSITE: PS00560; CARBOXYPEPT_SER_HIS; 1.
CC Hydrolase; Carboxypeptidase; Glycoprotein; Zymogen; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 73 BY SIMILARITY.
FT CHAIN 74 484 SERINE CARBOXYPEPTIDASE III.
FT PROPEP 485 500 BY SIMILARITY.
FT ACT_SITE 216 216 BY SIMILARITY.
FT ACT_SITE 404 404 BY SIMILARITY.
FT ACT_SITE 461 461 BY SIMILARITY.
FT BINDING 407 407 SUBSTRATE (BY SIMILARITY).
FT CARBOHYD 144 144 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 500 AA; 55446 MW; AE455E2780147DB8 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 500;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9
|||||:

Db 167 TGTGFSY 173

RESULT 8
CBP3_WHEAT
ID CBP3_WHEAT STANDARD; PRT; 500 AA.
AC P11515;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine carboxypeptidase III precursor (EC 3.4.16.5) (CP-WIII).
GN CBP3.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
NCBI_TaxID=4565;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=88007602; PubMed=2820978;
RA Baulcombe D.C., Barker R.F., Jarvis M.G.;
RT "A gibberellin responsive wheat gene has homology to yeast
RT carboxypeptidase Y.";
RL J. Biol. Chem. 262:13726-13735(1987).
CC -!- CATALYTIC ACTIVITY: Release of a C-terminal amino acid with a
CC broad specificity.
CC -!- SUBUNIT: MONOMER (PROBABLE).
CC -!- INDUCTION: BY GIBBERELIC ACID (GA).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.
CC
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CC
CC EMBL: J02817; AAA34273.1; -.
CC PIR: A29412; A29412.
CC HSSP: P00729; 1CPY.
CC MEROPS: S10.009; -.
CC InterPro: IPR000379; Ser_estrs.site.
CC ProDom: PD001189; Serine_carbpept. 1.
CC PROSITE: PS00131; CARBOXYPEPT_SER_SER; 1.
CC PROSITE: PS00560; CARBOXYPEPT_SER_HIS; 1.
CC Hydrolase; Carboxypeptidase; Glycoprotein; Zymogen; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 73 BY SIMILARITY.
FT CHAIN 74 484 SERINE CARBOXYPEPTIDASE III.
FT PROPEP 485 500 BY SIMILARITY.
FT ACT_SITE 216 216 BY SIMILARITY.
FT ACT_SITE 404 404 BY SIMILARITY.
FT ACT_SITE 461 461 BY SIMILARITY.
FT BINDING 407 407 SUBSTRATE (BY SIMILARITY).
FT CARBOHYD 144 144 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 500 AA; 55334 MW; B2ACE10EF8484CDA CRC64;

Query Match 72.0%; Score 36; DB 1; Length 500;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9
|||||:

RESULT 9
CBP3_HORVU
ID CBP3_HORVU STANDARD; PRT; 508 AA.

Db 174 TGTGFSY 180

RESULT 10
PHX5_MOUSE

ID	PHX5_MOUSE	STANDARD;	PRT;	672 AA.
AC	P08399;			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Per-hexamer repeat protein 5.			
GN	PHXR5 OR PER.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=86014384; PubMed=2413365;			
RX	Shin H.S., Baggiello T.A., Clark B.T., Jackson F.R., Young M.W.;			
RA	"An unusual coding sequence from a Drosophila clock gene is conserved			
RT	in vertebrates.";			
RL	Nature 317:445-448(1985).			
CC	-!- SIMILARITY: TO OTHER G-T STRETCH CONTAINING PROTEINS.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announcement/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M12039; AAA88320.1;			
DR	EMBL; X02966; CAA26710.1; ALT_INIT.			
DR	PIR; A24403; UMMS.			
DR	MGD; MGI:104521; Phxr5.			
DR	InterPro; IPR000561; EGF-like.			
DR	SMART; SM00181; EGF; 1.			
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.			
DR	Repeat.			
FT	DOMAIN 59 672 G-T REPEATS.			
SEQ	SEQUENCE 672 AA; 57924 MW; E85BF428CF424C0B CRC64;			
Query Match	70.0%; Score 35; DB 1; Length 672;			
Best Local Similarity	87.5%; Pred. No. 1.1e+02;			
Matches	7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
ID	VP4_ROTFC	STANDARD;	PRT;	736 AA.
AC	P26193;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)			
DE	[Contains: Outer capsid proteins VP5 and VP8].			
GN	S3.			
OS	Porcine rotavirus (group C / strain Cowden).			
OC	Viruses; dsRNA viruses; Reoviridae; Rotavirus.			
OX	NCBI_TaxID=10916;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92124743; PubMed=1310192;			
RA	Bremont M., Juste-Lesage P., Chabanne-Vautherot D.,			
RA	Charpallienne A., Cohen J.;			
RT	"Sequences of the four larger proteins of a porcine group C rotavirus			
RT	and comparison with the equivalent group A rotavirus proteins.";			

RL Virology 186:684-692(1992).
 CC -!- SUBCELLULAR LOCATION: Outer capsid.
 CC -!- PTM: VP8 IS ONE OF TWO TRYPSIN CLEAVAGE PRODUCTS OF VP4; THE
 CC OTHER PRODUCT IS VP5.
 CC -!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; M74218; AAB00802.1; -
 DR PIR: D40822; VPRXPC.
 DR InterPro: IPR000416; Cap_VP4.
 DR Pfam: PF00426; VP4; 1.
 KW Coat protein; Glycoprotein.
 FT CHAIN 1 736
 FT CHAIN 1 736
 FT CHAIN 1 736
 FT CARBOHYD 251 736
 FT CARBOHYD 39 736
 FT CARBOHYD 61 61
 FT CARBOHYD 64 64
 FT CARBOHYD 93 93
 FT CARBOHYD 162 162
 FT CARBOHYD 191 191
 FT CARBOHYD 237 237
 FT CARBOHYD 251 251
 FT CARBOHYD 304 304
 FT CARBOHYD 471 471
 FT CARBOHYD 631 631
 SQ SEQUENCE 736 AA; 83231 MW; 356F9226D5016577 CRC64;
 Query Match 70.08; Score 35; DB 1; Length 736;
 Best Local Similarity 85.78; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TGTGFAY 9
 :|||||
 DB 454 SGTGFAY 460
 RESULT 12
 VILLI_CHICK
 ID VILLI_CHICK STANDARD; PRT; 826 AA.
 AC P02640;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 OS Villin.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88276884; PubMed-2893826;
 RA Bazari W.L., Matsudaira P., Wallek M., Smeal T., Jakes R., Ahmed Y.;
 RT "Villin sequence and peptide map identify six homologous domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:4986-4990(1988).
 RN [2]
 RP SEQUENCE OF 751-826.
 RX MEDLINE-81264203; PubMed-6790532;
 RA Glenney J.R. Jr., Geisler N., Kaulfus P., Weber K.;
 RT "Demonstration of at least two different actin-binding sites in
 RT villin, a calcium-regulated modulator of F-actin organization.";
 RL J. Biol. Chem. 256:8156-8161(1981).
 RN [3]
 RP CALCIUM-BINDING SITES.
 RX MEDLINE-83082892; PubMed-6848508;

RA Hesterberg L.K., Weber K.;
 RT "Demonstration of three distinct calcium-binding sites in villin, a
 RT modulator of actin assembly.";
 RL J. Biol. Chem. 258:365-369(1983).
 RN [4]
 RP STRUCTURE BY NMR OF 1-127.
 RX MEDLINE-94191534; PubMed-8142900;
 RA Markus M.A., Nakayama T., Matsudaira P., Wagner G.;
 RT "Solution structure of villin 14T, a domain conserved among actin-
 RT severing proteins.";
 RL Protein Sci. 3:70-81(1994).
 RN [5]
 RP STRUCTURE BY NMR OF 1-127.
 RX MEDLINE-97337440; PubMed-9194180;
 RA Markus M.A., Matsudaira P., Wagner G.;
 RT "Refined structure of villin 14T and a detailed comparison with other
 RT actin-severing domains.";
 RL Protein Sci. 6:1197-1209(1997).
 RN [6]
 RP STRUCTURE BY NMR OF 792-826.
 RX MEDLINE-97307248; PubMed-9164455;
 RA McKnight C.J., Matsudaira P.T., Kim P.S.;
 RT "NMR structure of the 35-residue villin headpiece subdomain.";
 RL Nat. Struct. Biol. 4:180-184(1997).
 CC -!- FUNCTION: CA(2+)-REGULATED ACTIN-BINDING PROTEIN. ITS CAPPING
 CC FUNCTION IS LOCALIZED TO DOMAIN I; ITS SEVERING ACTION IS A
 CC COOPERATION BETWEEN AN F-ACTIN BINDING SITE OF DOMAIN II AND THE
 CC CAPPING ACTIVITY OF DOMAIN I.
 CC -!- SUBUNIT: MONOMER.
 CC -!- TISSUE SPECIFICITY: COMPONENT OF BRUSH BORDER MICROVILLI.
 CC -!- SIMILARITY: BELONGS TO THE VILLIN/GELSOLIN FAMILY.
 CC -!- SIMILARITY: CONTAINS 6 GELSOLIN-LIKE REPEATS.
 CC -----
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 CC -----
 CC EMBL; J03781; AAA49133.1; -
 DR PIR: A03082; A03082.
 DR PIR: A31822; A31822.
 DR PDB: 2VIL; 01-APR-97.
 DR PDB: 2VIL; 01-APR-97.
 DR PDB: 1VII; 12-AUG-97.
 DR InterPro: IPR001974; Gelsolin.
 DR InterPro: IPR003128; VHP.
 DR Pfam: PF00626; Gelsolin; 6.
 DR Pfam: PF02209; VHP; 1.
 DR PRINTS: PR00597; GELSOLIN.
 DR SMART: SM00262; GEL; 6.
 DR SMART: SM00153; VHP; 1.
 KW Cytoskeleton; Calcium; Actin-binding; Capping protein; Repeat;
 KW 3D-structure.
 RN DOMAIN 1 734
 FT DOMAIN 735 826
 FT REPEAT 27 76
 FT REPEAT 148 188
 FT REPEAT 265 309
 FT REPEAT 408 457
 FT REPEAT 528 568
 FT REPEAT 631 672
 FT SITE 820 823
 FT SITE 129 137
 FT SITE 112 119
 FT SITE 138 146
 FT STRAND 21 23
 FT STRAND 30 32
 FT TURN 34 36
 CORE.
 HEADPIECE.
 GELSOLIN-LIKE 1.
 GELSOLIN-LIKE 2.
 GELSOLIN-LIKE 3.
 GELSOLIN-LIKE 4.
 GELSOLIN-LIKE 5.
 GELSOLIN-LIKE 6.
 ABSOLUTELY REQUIRED FOR ACTIVITY.
 CRUCIAL FOR BINDING AN ACTIN FILAMENT.
 POLYPHOSPHONOSITIDE BINDING (BY
 SIMILARITY).
 POLYPHOSPHONOSITIDE BINDING (BY
 SIMILARITY).

FT STRAND 39 41
 FT STRAND 44 44
 FT STRAND 47 53
 FT STRAND 58 64
 FT STRAND 68 68
 FT HELIX 72 88
 FT TURN 89 90
 FT STRAND 95 97
 FT STRAND 104 110
 FT TURN 112 113
 FT STRAND 116 118
 FT TURN 124 125
 SQ SEQUENCE 826 AA; 6A8898F7DF947389 CRC64;

Query Match 70.0%; Score 35; DB 1; Length 826;
 Best Local Similarity 66.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 RGTGTGFAY 9
 | |||||
 52 RKTGSGFSY 60

RESULT 13

CYC_CHLRE STANDARD; PRT; 111 AA.

AC P15451;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cytochrome c.
 GN CYC1.
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadales; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=137C / CC-125, and cwl5;
 RX MEDLINE=89178731; PubMed=2853233;
 RA Anati B.B., Goldschmidt-Clermont M., Wallace C.J.A., Rochaix J.-D.;
 RT "cDNA and deduced amino acid sequences of cytochrome c from
 Chlamydomonas reinhardtii: unexpected functional and phylogenetic
 implications.";
 RT J. Mol. Evol. 28:151-160(1988).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=137C / CC-125;
 RX Felitti S.A., Chan R.L., Gonzalez D.H.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Electron carrier protein. The oxidized form of the
 cytochrome c heme group can accept an electron from the heme group
 of the cytochrome c1 subunit of cytochrome reductase. Cytochrome c
 then transfers this electron to the cytochrome oxidase complex,
 the final protein carrier in the mitochondrial electron-transport
 chain.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -!- PTM: Binds one heme group per molecule.
 CC -!- SIMILARITY: Belongs to the cytochrome c family.

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EMBL; M35173; AAA33084.1; -;
 EMBL; Z99829; CAB16954.1; -;
 PIR; S29514; S29514.
 HSSP; P00055; ICCR.
 InterPro; IPR000345; CytC_heme_bind.

DR InterPro; IPR003088; CYT_C1.
 DR InterPro; IPR002327; CYT_C1AB.
 DR Pfam; PF00034; cytochrome_c_1.
 DR PRINTS; PR00604; CYTCHRMCIAB.
 DR PRODOM; PD000375; CYT_C1AB; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; 1.
 KW Mitochondrion; Electron transport; Respiratory chain; Heme.
 FT INIT_MET 0
 FT BINDING 22 22 HEME (COVALENT).
 FT BINDING 25 25 HEME (COVALENT).
 FT METAL 26 26 IRON (HEME AXIAL LIGAND).
 FT METAL 88 88 IRON (HEME AXIAL LIGAND).
 SQ SEQUENCE 111 AA; 11826 MW; 6F11A35EA71C7078 CRC64;

Query Match 68.0%; Score 34; DB 1; Length 111;
 Best Local Similarity 75.0%; Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9
 || |||||
 DB 49 GTAGGFAY 56

RESULT 14

YOD2_CAEEL STANDARD; PRT; 233 AA.

AC P34594;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical 26.8 kDa protein ZC262.2 in chromosome III.
 GN ZC262.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
 Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A.,
 Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
 Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
 Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 Parsons J., Percy C., Rifkin L., Ropra A., Saunders D., Showkeen R.,
 Sims M., Smaldon N., Smith A., Smith M., Sonnenhammer E., Staden R.,
 Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 CC -----
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EMBL; L23647; AAK29991.1; -;
 PIR; S44882; S44882.
 WormPep; ZC262.2; CE00350.
 KW Hypothetical protein.
 SQ SEQUENCE 233 AA; 26825 MW; 84F99FB67A6DD5D6 CRC64;

Query Match 68.0%; Score 34; DB 1; Length 233;
 Best Local Similarity 66.7%; Pred. No. 60;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

	PRINTS; PR00167; CACHANNEL.		
DR	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;		
KW	Calcium channel; Glycoprotein; Repeat; Multigene family;		
KW	Calcium-binding; Phosphorylation.		
FT	NON_TER I	<1	8 III.
FT	REPEAT	45	>281 IV.
FT	TRANSMEM	<1	S6 OF REPEAT III (POTENTIAL).
FT	DOWAIN	6	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	59	S1 OF REPEAT IV (POTENTIAL).
FT	DOWAIN	78	S2 OF REPEAT IV (POTENTIAL).
FT	TRANSMEM	93	CYTOPLASMIC (POTENTIAL).
FT	DOWAIN	113	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	121	S3 OF REPEAT IV (POTENTIAL).
FT	DOWAIN	140	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	153	S4 OF REPEAT IV (POTENTIAL).
FT	DOWAIN	172	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	191	S5 OF REPEAT IV (POTENTIAL).
FT	DOWAIN	211	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	278	S6 OF REPEAT IV (POTENTIAL).
FT	BINDING	<1	TO DIHYDROPYRIDINES (BY SIMILARITY).
FT	BINDING	258	TO DIHYDROPYRIDINES (BY SIMILARITY).
FT	BINDING	270	TO PHENYLALKYLAMINES (BY SIMILARITY).
FT	SITE	244	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	CARBONYD	81	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	NON_TER	281	
SQ	SEQUENCE	281 AA; 32729 MW; 46BE70FAA4D9166B CRC64;	
	Query Match	68.0%; Score 34; DB 1; Length 281;	
	Best Local Similarity	100.0%; Pred. No. 71;	
	Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	GTGFAY 9		
Db	274 GTGFAY 279		

Search completed: February 14, 2003, 11:16:21
Job time : 5.64516 secs

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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:10:17 : Search time 18.7258 Seconds
(without alignments)
99.030 Million cell updates/sec

Title: US-09-701-001B-3
Perfect score: 50
Sequence: 1 RGTGTGFAY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Sorted: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	41	82.0	416	Q8XT81	Q8xt81 ralstonia s
2	39	78.0	644	Q83342	Q83342 murid herpe
3	39	78.0	644	Q41940	Q41940 murid herpe
4	39	78.0	685	Q8RNT4	Q8rnt4 pseudomonas
5	39	78.0	685	Q914G8	Q914g8 pseudomonas
6	37	74.0	266	Q42245	Q42245 brachydanio
7	37	74.0	502	Q8XVU9	Q8xyvu9 anabaena sp
8	37	74.0	519	Q93J30	Q93j30 streptomyc
9	36	72.0	101	Q41689	Q41689 vigna radia
10	36	72.0	146	Q92TR3	Q92tr3 hordeum vul
11	36	72.0	150	Q41601	Q41601 triticum tu
12	36	72.0	165	Q40651	Q40651 oryza sativ
13	36	72.0	198	Q8XIF4	Q8xfi4 clostridium
14	36	72.0	360	Q9M450	Q9m450 cicer ariet
15	36	72.0	401	Q96ZK7	Q96zk7 sulfolobus
16	36	72.0	423	Q91201	Q91201 pseudomonas

17	36	72.0	482	5	Q9TY20	Q9ty20 plasmodium
18	36	72.0	501	10	Q9XH61	Q9xh61 matricaria
19	36	72.0	1077	16	Q92U15	Q92u15 rhizobium m
20	36	72.0	3295	16	Q8Z1A8	Q8zia8 rhizobium pe
21	35	70.0	163	16	Q90UH9	Q90uh9 staphylococ
22	35	70.0	398	16	Q930R4	Q930r4 rhizobium m
23	35	70.0	401	16	Q8YLY2	Q8yly2 anabaena sp
24	35	70.0	429	16	Q8YLY2	Q8yly2 anabaena sp
25	35	70.0	440	16	Q9RXX0	Q9rxx0 streptomyce
26	35	70.0	452	16	P73354	P73354 synechocyst
27	35	70.0	563	4	O60398	O60398 homo sapien
28	35	70.0	579	2	O8VLY0	O8vly0 treponema s
29	35	70.0	733	12	Q65525	Q65525 bovine grou
30	35	70.0	744	12	Q82039	Q82039 human rotav
31	35	70.0	744	12	Q82040	Q82040 human rotav
32	35	70.0	744	12	Q993A0	Q993a0 human rotav
33	35	70.0	744	12	Q99229	Q992z9 human rotav
34	35	70.0	744	12	Q8V9B0	Q8v9b0 human rotav
35	35	70.0	747	4	Q13311	Q13311 homo sapien
36	35	70.0	747	4	Q9U188	Q9u188 homo sapien
37	35	70.0	758	5	O9NKT0	O9nkt0 leishmania
38	35	70.0	789	4	O9BQG5	O9bqg5 homo sapien
39	35	70.0	2115	17	Q8TQ00	Q8tqn0 methanosarc
40	34	68.0	41	2	O9ZG78	O9zg78 chlamydia t
41	34	68.0	99	16	O9PE10	O9pel0 xylella fas
42	34	68.0	110	2	Q9AQH8	Q9aqm8 pseudomonas
43	34	68.0	134	10	O9FKF5	O9fkf5 arabidopsis
44	34	68.0	134	10	O945L5	O945l5 arabidopsis
45	34	68.0	149	13	Q8UVC7	Q8uvc7 agkistrodon

ALIGNMENTS

RESULT 1
Q8XT81
ID Q8XT81 PRELIMINARY; PRT; 416 AA.
AC Q8XT81;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Probable metabolite transport transmembrane protein.
GN RSP0234 OR RS05189.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siquier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RL Nature 415:497-502(2002).
RL "Genome sequence of the plant pathogen Ralstonia solanacearum.";
DR EMBL; AL646077; CAD17385.1; --
DR InterPro; IPR003662; sub.transporter.
DR Pfam; PF00083; sugar_tr; 1
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
KW Plasmid; Complete proteome.
SQ SEQUENCE 416 AA; 44052 MW; 4AC593FD3AC0EF4B CRC64;

Query Match 82.0%; Score 41; DB 16; Length 416;
Best Local Similarity 77.8%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 RGTGTGFAY 9

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||||| ||| |
Db 350 RGTGVCFCY 358

RESULT 2
Q83342
AC Q83342 PRELIMINARY; PRT: 644 AA.
ID Q83342;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Thymidine kinase.
OS murid herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gamaherpesvirinae.
OX NCBI_TaxID=33708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G2.4;
RX MEDLINE=96213518; PubMed=8638414;
Pepper S.D., Stewart J.P., Arrand J.R., Mackett M.;
"Murine gammaherpesvirus-68 encodes homologues of thymidine kinase and
glycoprotein H: sequence, expression, and characterization of
pyrimidine kinase activity.";
Virology 219:475-479(1996).
RL EMBL: X93468; CAA63755.1; -.
DR EMBL: X93468; CAA63755.1; -.
DR InterPro: IPR001889; TK_herpes.
DR Pfam: PF00693; TK_herpes; 1.
DR ProDom: PD001519; TK_herpes; 1.
KW Kinase.
SQ SEQUENCE 644 AA; 72256 MW; FDF782746EB557A9 CRC64;

Query Match 78.0%; Score 39; DB 12; Length 644;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9
Db 300 RGDGTGFY 308
|||||

RESULT 3
Q41940
AC Q41940 PRELIMINARY; PRT: 644 AA.
ID Q41940;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Thymidine kinase.
OS murid herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gamaherpesvirinae.
OX NCBI_TaxID=33708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WUMS, AND G2.4;
RX MEDLINE=97366649; PubMed=9223479;
Virgin H.W. IV, Latreille P., Wamsley P., Hallsworth K., Weck K.E.,
Dal Canto A.J., Speck S.H.;
"Complete sequence and genomic analysis of murine gammaherpesvirus
68.";
Virology 219:475-479(1996).
RL J. Virol. 71:5894-5904(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WUMS;
RX MEDLINE=96213518; PubMed=8638414;
Latreille P., Wamsley P., Waterston R.H.;
Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=G2.4;
RX MEDLINE=96213518; PubMed=8638414;
Pepper S.D., Stewart J.P., Arrand J.R., Mackett M.;

"Murine gammaherpesvirus-68 encodes homologues of thymidine kinase and
glycoprotein H: sequence, expression, and characterization of
pyrimidine kinase activity.";
Virology 219:475-479(1996).
RL EMBL: U97553; AAB66394.1; -.
DR EMBL: AF105037; AAF19286.1; -.
DR InterPro: IPR001889; TK_herpes.
DR Pfam: PF00693; TK_herpes; 1.
DR ProDom: PD001519; TK_herpes; 1.
KW Kinase.
SQ SEQUENCE 644 AA; 72269 MW; FD3CD1646F6E5562 CRC64;

Query Match 78.0%; Score 39; DB 12; Length 644;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9
Db 300 RGDGTGFY 308
|||||

RESULT 4
Q8RNT4
ID Q8RNT4 PRELIMINARY; PRT: 685 AA.
AC Q8RNT4;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Linoleate oxygen oxidoreductase.
GN LOX.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=42A2 NCBI 40045;
RA Vidal-Mas J., Besumbes O., Manresa M., Busquets M.;
"Cloning, sequence and expression of a lipoygenase gene of
Pseudomonas aeruginosa 42A2 NCBI 40045.";
Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF479686; AAL85880.1; -.
DR EMBL: AF479686; AAL85880.1; -.
SQ SEQUENCE 685 AA; 74572 MW; DA863B58A47C4C29 CRC64;

Query Match 78.0%; Score 39; DB 2; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9
Db 305 TGTGFAY 311
|||||

RESULT 5
Q9I4G8
ID Q9I4G8 PRELIMINARY; PRT: 685 AA.
AC Q9I4G8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Probable lipoygenase.
GN PALL69.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoquchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.D., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
RL EMBL; AE004547; AAG04558.1; -;
DR HSP; P08170; 2SBL.
DR InterPro: IPR000907; Lipoxigenase.
DR Pfam: PF00305; lipoxigenase; 1.
DR PRINTS: PR00087; LIPOXYGENASE.
KW Complete proteome.
SQ SEQUENCE 685 AA; 74803 MW; B6A307595AE16A5E CRC64;

Query Match 78.0%; Score 39; DB 16; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGTFAY 9
|||||
DB 305 TGTGTFAY 311

RESULT 6
ID O42245 PRELIMINARY; PRT; 266 AA.
AC O42245;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Atonal homologue-1.
GN ATOH1 OR ZATH-1.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim C.-H., Bae Y.-K., Yamanaka Y., Yamashita S., Shimizu T., Fujii R.,
RA Hibi M., Hirano T.;
RA Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
EMBL; AF024536; AAB82272.1; -;
DR ZFIN; ZDB-GENE-990415-17; atoh1.
DR InterPro: IPR001092; HLH_basic.
DR Pfam: PF00010; HLH; 1.
DR SMART: SM00353; HLH; 1.
SQ SEQUENCE 266 AA; 28786 MW; 56A92494B52FEFB8 CRC64;

Query Match 74.0%; Score 37; DB 13; Length 266;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTFAY 9
|||||
DB 209 RGTGTFAY 217

RESULT 7
ID Q8YVU9 PRELIMINARY; PRT; 502 AA.
AC Q8YVU9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein A11875.
GN A11875.

OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium *Anabaena* sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003587; BAB73574.1; -;
DR InterPro: IPR004843; M-peptidase.
DR InterPro: IPR004844; S/T-phosphatase.
DR Pfam: PF00149; Metallophos; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 502 AA; 57518 MW; A5F008C8C2C59E61 CRC64;

Query Match 74.0%; Score 37; DB 16; Length 502;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTFAY 9
|||||
DB 159 RGTGTFAY 167

RESULT 8
ID Q93J30 PRELIMINARY; PRT; 519 AA.
AC Q93J30;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative protease
GN SCO3977 OR SCBAC25E3.14.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Collins M., Harris D.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RL the 8 Mb *Streptomyces coelicolor* A3(2) chromosome.";
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabbinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,

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RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RL coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL596251; CAC44701.1; -.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00089; trypsin; 1.
DR Hydrolase; Protease; Serine protease.
SQ SEQUENCE 519 AA; 50327 MW; 5CB9D5F0CC19E428 CRC64;

Query Match 74.0%; Score 37; DB 16; Length 519;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9
Db 228 GTGTGFVF 235
|||||
228 GTGTGFVF 235

RESULT 9
Q41689
ID Q41689 PRELIMINARY; PRT; 101 AA.
AC Q41689;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Carboxypeptidase II (fragment).
OS Vigna radiata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=157791;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JUMBO; TISSUE=COTYLEDONS;
RA Lee K., Tan-Wilson A.L., Wilson K.A.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U49382; AAA92062.1; -.
DR HSP; P08819; IWHI.
DR InterPro; IPR001563; Serine_carbpept.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00450; serine_carbpept; 1.
DR PRINTS; PR00724; CRBOXYPASEC.
DR ProDom; PD001189; Serine_carbpept; 1.
DR PROSITE; PS00131; CARBOXYPEPT_SER_SER; 1.
FT NON_TER 1
NON_TER 101 101
SEQUENCE 101 AA; 11467 MW; 40E371DBB2D53818 CRC64;

Query Match 72.0%; Score 36; DB 10; Length 101;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9
Db 49 TGTGFYSY 55
|||||
49 TGTGFYSY 55

RESULT 10
Q9ZTR3
ID Q9ZTR3 PRELIMINARY; PRT; 146 AA.
AC Q9ZTR3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Dehydrin 9.
GN DHN9.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.

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OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DICKTOO;
RA Choi D.-W., Zhu B., Close T.J.;
RT "The barley (Hordeum vulgare L.) dehydrin multigene family: sequences,
RT chromosome assignments, and expression characteristics of 11 dhv genes
RT of cv. Dicktoo.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MOREX;
RA Choi D.-W., Close T.J.;
RT "Morex barley (Hordeum vulgare L. cv. Morex) dehydrin multigene
RT family.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF043094; AAD02260.1; -.
DR EMBL; AF181459; AAF01697.1; -.
DR InterPro; IPR000167; Dehydrin.
DR Pfam; PF00257; dehydrin; 1.
DR PROSITE; PS00315; DEHYDRIN_1; 1.
DR PROSITE; PS00823; DEHYDRIN_2; 2.
SQ SEQUENCE 146 AA; 15128 MW; B979904F6800E299 CRC64;

Query Match 72.0%; Score 36; DB 10; Length 146;
Best Local Similarity 87.5%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9
Db 100 GTGTGGAY 107
|||||
100 GTGTGGAY 107

RESULT 11
Q41601
ID Q41601 PRELIMINARY; PRT; 150 AA.
AC Q41601;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Dehydrin.
OS Triticum turgidum subsp. durum (durum wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4567;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SILIANA; TISSUE=DEHYDRATED ROOT;
RA Labhili M., Joudrier PH., Gautier M.F.;
RT "Characterization of cDNAs encoding Triticum durum dehydrins and their
RT expressions patterns in cultivars that differ in drought tolerance.";
RL Plant Sci. 112:219-230(1995).
DR EMBL; X78431; CAA55194.1; -.
DR InterPro; IPR000167; Dehydrin.
DR Pfam; PF00257; dehydrin; 1.
DR PROSITE; PS00315; DEHYDRIN_1; 1.
DR PROSITE; PS00823; DEHYDRIN_2; 2.
SQ SEQUENCE 150 AA; 15163 MW; 3F3C846F526E03F8 CRC64;

Query Match 72.0%; Score 36; DB 10; Length 150;
Best Local Similarity 87.5%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9
Db 100 GTGTGGAY 107
|||||
100 GTGTGGAY 107

RESULT 12
Q40651
ID Q40651 PRELIMINARY; PRT; 165 AA.
AC Q40651;

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DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Dehydrin.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoidae; Oryzeae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McEvoy S.M., Sheoran I.S., Saini H.S.;
 RT "A rice cDNA encoding a late embryogenesis abundant protein.";
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U60097; AAB03330.1; -;
 DR InterPro; IPR000167; Dehydrin.
 DR Pfam; PF00257; dehydrin.1.
 DR PROSITE; PS00823; DEHYDRIN.2; 1.
 DR SEQUENCE 165 AA; 16671 MW; 581218E22BE37043 CRC64;
 Query Match 72.0%; Score 36; DB 10; Length 165;
 Best Local Similarity 87.5%; Pred. No. 83;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GTGTGFAY 9
 Db 116 GTGTGGAY 123
 RESULT 13
 Q8X1F4 PRELIMINARY; PRT; 198 AA.
 ID Q8X1F4;
 AC Q8X1F4;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein CPE2167.
 GN CPE2167.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OC NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-13 / TYPE A;
 RX PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yanashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 flesh-eater."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL; AF003193; BAB81873.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 198 AA; 21538 MW; E5E6F630D8434332 CRC64;
 Query Match 72.0%; Score 36; DB 16; Length 198;
 Best Local Similarity 85.7%; Pred. No. 1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGTGTGF 7
 Db 74 KGTGTGF 80
 RESULT 14
 Q9M450 PRELIMINARY; PRT; 360 AA.
 ID Q9M450;
 AC Q9M450;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Serine carboxypeptidase (EC 3.4.16.6) (Fragment).
 OS Cicer arietinum (Chickpea) (garbanzo).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
 OC NCBI_TaxID=3827;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-CV. CASTELLANA; TISSUE=ETIOLATED EPICOTYLS;
 RA Dopico B., Esteban R., Labrador E.;
 RT "A serine carboxypeptidase is expressed in chickpea epicotyls.";
 RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AJ271659; CAB71127.1; -;
 DR HSSP; P08819; 1BCS.
 DR MEROPS; S10.009; -;
 DR InterPro; IPR001563; Serine_carbpept.
 DR Pfam; PF00450; serine_carbpept.1.
 DR PRINTS; PR00724; CRBOXYPTASEC.
 DR PRODOM; PD001189; Serine_carbpept.1.
 DR PROSITE; PS00560; CARBOXYPEPT_SER_HIS; 1.
 DR PROSITE; PS00131; CARBOXYPEPT_SER_SER; 1.
 KW Carboxypeptidase; Hydrolase.
 FT NON_TER 1
 SQ SEQUENCE 360 AA; 40153 MW; 140BEBACD0143FE0 CRC64;
 Query Match 72.0%; Score 36; DB 10; Length 360;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TGTGFAY 9
 Db 29 TGTGFSY 35
 RESULT 15
 Q96ZK7 PRELIMINARY; PRT; 401 AA.
 ID Q96ZK7;
 AC Q96ZK7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Putative transporter.
 GN ST1828.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OC NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JCM 10545 / 7;
 RX PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Ohshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermoacidophilic
 Crenarchaeon, Sulfolobus tokodaii strain 7.";
 RL DNA Res. 8:123-140(2001).
 DR EMBL; AP000987; BAB66918.1; -;
 DR InterPro; IPR003662; sub.transporter.
 DR Pfam; PF00083; sugar_tr.1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 401 AA; 43730 MW; 73BE08EA26463B17 CRC64;
 Query Match 72.0%; Score 36; DB 17; Length 401;
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RGTGTGFAY 9
 Db 336 RATGVTGFSY 344

Fri Feb 14 15:00:54 2003

us-09-701-001b-3.rspt

Page 6

Search completed: February 14, 2003, 11:18:39
Job time : 20.8925 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:04:17 : Search time 40.6452 Seconds
(without alignments)
49.176 Million cell updates/sec

Title: US-09-701-001B-4

Perfect score: 79

Sequence: 1 KASQSVYDGDGYMN 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Search: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
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- 18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	79	100.0	15	AA70195	MAB 3B9 light chain
2	79	100.0	15	AAW3027	Anti-Fas MAB HFE/A
3	79	100.0	15	AA23772	CDR of the light c
4	79	100.0	15	AA18114	Light chain CDR fo
5	79	100.0	15	AA14744	Mouse anti-Fas ant
6	79	100.0	15	AAW90894	Murine anti-Fas an
7	79	100.0	15	AA59259	Antibody 4H5 L cha
8	79	100.0	15	AA51136	Murine CD4/CD34 re
9	79	100.0	15	ABB74863	Humanised anti-Fas
10	79	100.0	15	ABB74909	Humanised anti-Fas

11	79	100.0	19	AA66143	CD-4 antibody vari
12	79	100.0	103	AA59263	Antibody 4H5 L cha
13	79	100.0	103	AA51140	Murine derived pro
14	79	100.0	106	AA33309	MAE15 light chain.
15	79	100.0	106	AA51197	Light chain amino
16	79	100.0	111	AA90541	Immunoglobulin L c
17	79	100.0	111	AA33305	MAE11 light chain.
18	79	100.0	111	AA55123	Mouse anti-HIV mu5
19	79	100.0	111	AA55127	Mouse-human chimera
20	79	100.0	111	AA60302	Anti HIV antibody
21	79	100.0	111	AA60306	Chimeric anti HIV
22	79	100.0	111	AA23781	Light chain variab
23	79	100.0	111	AA18123	Light chain sequen
24	79	100.0	111	AAW5650	Mus musculus anti-
25	79	100.0	111	AA55193	Light chain amino
26	79	100.0	111	AA59267	Antibody 4H5 L cha
27	79	100.0	111	AA51144	Murine derived pro
28	79	100.0	111	AA51146	Murine derived pro
29	79	100.0	111	AA76939	Variable light cha
30	79	100.0	112	AA24575	Human x mouse modi
31	79	100.0	113	AA71895	Monoclonal antibod
32	79	100.0	115	AA04134	Anti-Leu 3a light
33	79	100.0	120	AA48618	Sequence of the mo
34	79	100.0	131	AA90543	Amino acids sequen
35	79	100.0	131	AA04132	Anti-Leu 3a light
36	79	100.0	131	AA75355	Humanized antibody
37	79	100.0	131	AA70202	Humanized antibody
38	79	100.0	131	AA23779	Light chain variab
39	79	100.0	131	AA23771	Light chain variab
40	79	100.0	131	AA18126	Light chain sequen
41	79	100.0	131	AA18118	Light chain sequen
42	79	100.0	132	AA70189	Mouse MAB 3B9 ligh
43	79	100.0	132	AA23767	Light chain variab
44	79	100.0	132	AA18120	Light chain sequen
45	79	100.0	218	AA13563	Humanised anti-L-s

ALIGNMENTS

RESULT 1
AA70195
ID AA70195 standard; Protein; 15 AA.
XX
AC AA70195;
XX 20-SEP-1995 (first entry)
DT MAB 3B9 light chain CDR.
XX
DE Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; MAB; interleukin-4; IL-4; allergy; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9507301-A.
XX
PD 16-MAR-1995.
XX
PF 07-SEP-1994; 94WO-US10308.
XX
PR 07-SEP-1993; 93US-0117366.
PR 14-OCT-1993; 93US-0136783.
XX
(SMIK) SMITHKLINE BEECHAM CORP.
XX (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
XX WPI; 1995-123387/16.
XX
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived

PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions

XX
 PS Disclosure; Page 54; 97pp; English.

CC Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
 CC chains were cloned into pGEM7f+ and transformed into E. coli
 CC DH5-alpha. A light chain cDNA clone was sequenced (AA083490) that
 CC encoded the protein given in AAR70189. 3 CDRs (AAR70195-97) were
 CC identified.

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDDYDGD SYMN 15
 |||||
 Db 1 KASQSVDDYDGD SYMN 15

RESULT 2

AAW83027
 ID AAW83027 standard; Peptide; 15 AA.

XX AC AAW83027;

XX DT 15-MAR-1999 (first entry)

XX DE Anti-Fas MAb HFE7A light chain CDR-I1.

XX KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; complementarity determining region;
 KW CDR.

XX OS Mus musculus.

XX AU9859701-A.

PD 08-OCT-1998.

PF 30-MAR-1998; 98AU-0059701.

XX 08-OCT-1997; 97JP-0276064.

PR 01-APR-1997; 97JP-0082953.

PR 25-JUN-1997; 97JP-0169088.

PA (SANY) SANKYO CO LTD.

XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

PI Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX WPI; 1998-543440/47.

XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS

XX Claim 9; Page 184; 292pp; English.

CC This is the amino acid of complementarity determining region 1
 CC (CDR-I1) of the light chain (see AAW83042) of murine anti-human Fas
 CC monoclonal antibody HFE7A. The invention relates to antibodies,
 CC especially humanised antibodies (see AAW83031-37), recognising the
 CC Fas antigen. Such antibodies preferably comprise a heavy chain and
 CC a light chain including CDRs (see AAW83024-29) from the heavy and
 CC light chains of HFE7A. Humanised antibodies are produced by CDR
 CC grafting. The antibodies are capable of inducing apoptosis in
 CC abnormal cells expressing Fas, and of inhibiting Fas-induced
 CC apoptosis in normal cells. They are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's
 CC disease, thrombopenia purpura and insulin-dependent diabetes),
 CC allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and
 CC transplant rejection (all claimed).

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 19; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDDYDGD SYMN 15

|||||

Db 1 KASQSVDDYDGD SYMN 15

RESULT 3

AAV23772
 ID AAV23772 standard; Peptide; 15 AA.

XX AC AAV23772;

XX DT 13-SEP-1999 (first entry)

XX DE CDR of the light chain variable region of antibody 3B9.

XX KW Light chain variable region; Interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;
 KW allergy; complementarity determining region.

XX OS Mus sp.

XX US5928904-A.

PD 27-JUL-1999.

PF 07-JUN-1995; 95US-0483632.

XX 07-JUN-1995; 95US-0483632.

PR 07-SEP-1993; 93US-0117366.

PR 14-OCT-1993; 93US-0136783.

PR 07-SEP-1994; 94WO-US10308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1999-429500/36.

XX N-PSDB; AAX85889.

XX New DNA molecules encoding recombinant antibodies useful for
 PT treating IL4-mediated conditions

XX Example 3; Column 43-44; 50pp; English.

XX The present sequence represents a complementarity determining region

XX (CDR) of the light chain variable region of murine interleukin-4

XX (IL-4) antibody 389. The specification describes chimeric and

XX humanised IL-4 monoclonal antibodies. The antibodies of the

XX invention are used in therapeutic and pharmaceutical compositions

XX for treating IL-4 mediated and immunoglobulin E-mediated allergic

XX reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis,

XX atopic asthma, anaphylactic shock, rheumatoid arthritis,

XX host-versus-graft disease and renal disease. They are also useful

XX in the diagnosis of an allergy or condition associated with excess

XX IL-4 production through the measurement e.g. by ELISA of circulating

XX endogenous IL-4 levels in humans.

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 20; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGDSDYMN 15

DB 1 KASQSVDDYDGDSDYMN 15

|||||

RESULT 4

AA18114

ID AAY18114 standard; peptide; 15 AA.

XX AAY18114;

XX 11-AUG-1999 (first entry)

XX Light chain CDR for hIL-4 specific antibody.

XX Antibody; Interleukin-4; IL4; Immunoglobulin E; IgE mediated disease;

XX allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;

XX atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;

XX autoimmune disease; graft versus host disease;

XX complementarity determining region; CDR.

XX Synthetic.

XX US914110-A.

XX 22-JUN-1999.

XX 07-JUN-1995; 95US-0483636.

XX 07-JUN-1995; 95US-0483636.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX 07-SEP-1994; 94WO-US10308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1999-370482/31.

XX N-PSDB; AAX79513.

XX Recombinant IL4 antibodies

XX Claim 7; Column 43; 50pp; English.

XX This sequence represents a light chain complementarity determining region

XX (CDR) from an antibody of the invention. The antibody is a chimeric or

XX humanised interleukin-4 (IL4) monoclonal antibody for the treatment of

XX immunoglobulin E (IgE) mediated diseases. The antibodies are useful for

XX the treatment of allergic disorders such as allergic rhinitis,

CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.

CC The antibodies are also useful for regulating B and T cell proliferation

CC and as such are useful in the treatment of autoimmune diseases and graft

CC versus host disease.

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 20; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGDSDYMN 15

DB 1 KASQSVDDYDGDSDYMN 15

|||||

RESULT 5

AAB14744

ID AAB14744 standard; peptide; 15 AA.

XX AAB14744;

XX 24-NOV-2000 (first entry)

XX Mouse anti-Fas antibody HFE7A light chain CDR1.

XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;

XX murine; complementarity determining region; CDR; human Fas;

XX Fas ligand; apoptosis modulator; programmed cell death;

XX autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;

XX cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;

XX hepatitis; AIDS; graft rejection; light chain.

XX Mus musculus.

XX JP2000169393-A.

XX 20-JUN-2000.

XX 30-SEP-1999; 99JP-0278301.

XX 30-SEP-1999; 98JP-0276883.

XX (SANY) SANKYO CO LTD.

XX WPI; 2000-485645/43.

XX Preventive or treating agent for the diseases caused by an abnormality

XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains

XX anti-Fas antibody .

XX Claim 10; Page 65; 139pp; Japanese.

XX The invention relates to compositions for the prevention or treatment

XX or diseases caused by an abnormality in the Fas/Fas ligand system

XX containing an anti-Fas antibody as the active component. The anti-Fas

XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,

XX or a humanised version of HFE7A containing identical CDRs

XX (complementarity determining regions) to antibody HFE7A. Via its

XX interaction with Fas, the antibody of the invention acts as a modulator

XX of apoptosis. The composition of the invention may therefore be used in

XX the treatment or prevention of conditions such as autoimmune diseases,

XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,

XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS

XX and organ graft rejection. Sequences AAB14744-B14746 represent CDRs 1-3

XX of the light chain of the murine anti-human Fas monoclonal antibody

XX HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828).

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 21; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15
 |||||
 Db 1 KASQSVVDYDGD SYMN 15

RESULT 6
 AA90894
 ID AA90894 standard; peptide; 15 AA.
 XX
 AC AA90894;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Murine anti-Fas antibody peptide fragment #4.
 XX
 KW Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Mus musculus.
 XX EP990663-A2.
 XX
 PN 05-APR-2000.
 XX
 PD 29-SEP-1999; 99EP-0307711.
 XX
 PF 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI; 2000-258930/23.
 DR
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX

Disclosure; Page 98; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in

CC murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a murine anti-Fas antibody peptide fragment described in the method of the invention.

XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 79; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15
 |||||
 Db 1 KASQSVVDYDGD SYMN 15

RESULT 7
 AA59259
 ID AA59259 standard; peptide; 15 AA.
 XX
 AC AA59259;
 XX
 DT 17-APR-2000 (first entry)
 XX
 DE Antibody 4H5 L chain variable region CDR1 fragment.
 XX
 KW CD4 antigen; anti-human; antibody; 4H5; drug; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX JP11332563-A.
 XX
 PN 07-DEC-1999.
 PD
 XX
 PF 26-MAY-1998; 98JP-0163034.
 PR 26-MAY-1998; 98JP-0163034.
 XX
 PA (ASAH) ASahi Kasei Kogyo KK.
 XX WPI; 2000-091351/08.
 DR
 XX
 PT An antibody and the nucleic acid coding the antibody -
 XX
 PS Claim 2; Page 14; 25pp; Japanese.
 XX

The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. Sequences AA59259-61 represent the complementarity determining region (CDR)-1, CDR-2 and CDR-3 fragments in the L chain variable region of the antibody 4H5 respectively.

XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 79; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15
 |||||
 Db 1 KASQSVVDYDGD SYMN 15

RESULT 8
 AA51136
 ID AA51136 standard; Protein; 15 AA.
 XX
 AC AA51136;
 XX
 DT 31-MAR-2000 (first entry)

XX DE Murine CD4/CD34 recognizing antibody light chain CDR-1 region #1.
 XX KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 XX KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 XX KW HIV infection; autoimmune disease; complementarity determining region;
 XX KW CDR-1; light chain; murine.
 XX OS Mus sp.
 XX PN WO9961629-A1.
 XX PD 02-DEC-1999.
 XX PF 24-MAY-1999; 99WO-JP02711.
 XX PR 25-MAY-1998; 98JP-0159957.
 XX PR 26-MAY-1998; 98JP-0163023.
 XX (ASAH) ASAH KASEI KOGYO KK.
 XX (ASAH) ASAH MEDICAL CO LTD.
 XX Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI; 2000-086720/07.
 XX Devices containing antibodies recognising CD4 or CD34 and their use for
 XX the separation of CD4 or CD34 positive cells -
 XX Claim 3; Page 76; 11lpp; Japanese.
 XX This invention describes a novel device (I) for separating cluster
 XX differentiation (CD)-positive cells using a recombinant (chimeric or
 XX single-chain) antibody recognising CD4 or CD34. The devices are useful
 XX for the separation of CD4 or CD34 positive cells, which is useful for
 XX the collection of hematopoietic undifferentiated cells, elimination of
 XX lymphocytes from cells to be used in bone marrow transplantation, the
 XX detection of leukemic cells and the production of medicinal
 XX compositions for the treatment of HIV infection and autoimmune diseases.
 XX This sequence represents a murine derived complementarity determining
 XX region CDR-1 protein fragment which is used to illustrate the method of
 XX the invention.
 XX SQ Sequence 15 AA;
 Query Match 100.0%; Score 79; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. NO. 1.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVYDGDSDSYMN 15
 |||||
 DB 1 KASQSVYDGDSDSYMN 15
 |||||
 RESULT 9
 ABB74863
 ID ABB74863 standard; Peptide; 15 AA.
 XX AC ABB74863;
 XX 26-APR-2002 (first entry)
 XX Humanised anti-Fas antibody related peptide SEQ ID NO 29.
 XX Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
 XX light chain subunit; apoptosis; immunosuppressive; antiallergic;
 XX autoimmune disease; allergy; atopic.
 XX OS Homo sapiens.
 XX PN JP2001342148-A.
 XX PD 11-DEC-2001.
 XX Query Match 100.0%; Score 79; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. NO. 1.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVYDGDSDSYMN 15
 |||||
 DB 1 KASQSVYDGDSDSYMN 15
 |||||
 RESULT 9
 ABB74863
 ID ABB74863 standard; Peptide; 15 AA.
 XX AC ABB74863;
 XX 26-APR-2002 (first entry)
 XX Humanised anti-Fas antibody related peptide SEQ ID NO 29.
 XX Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
 XX light chain subunit; apoptosis; immunosuppressive; antiallergic;
 XX autoimmune disease; allergy; atopic.
 XX OS Homo sapiens.
 XX PN JP2001342148-A.
 XX PD 11-DEC-2001.

XX PF 28-MAR-2001; 2001JP-0093106.
 XX PR 29-MAR-2000; 2000JP-0090918.
 XX PA (SANY) SANKYO CO LTD.
 XX WPI; 2002-145113/19.
 XX Drug containing humanised anti-Fas antibody, used for preventing and
 XX treating autoimmune diseases, allergy, and atopy -
 XX Example 6 (Preparatory); Page 26; 194pp; Japanese.
 XX The invention relates to a preventive or treating agent for diseases
 XX caused by abnormality in Fas/Fas ligand system containing as the active
 XX component an antibody having as the light chain subunit a polypeptide
 XX containing residues 1-218 of one of 3, 239 residue amino acid sequences,
 XX or residues 1-451 of one of 3, 470 residue amino acid sequences, all
 XX fully defined in the specification and having an activity of combining
 XX specifically with mammalian Fas and an activity of inducing apoptosis
 XX in a cell expressing Fas. The agent has immunosuppressive and
 XX antiallergic activity and is used for preventing and treating autoimmune
 XX diseases, allergy, atopy and others. The present sequence is that of a
 XX peptide, useful to the invention.
 XX SQ Sequence 15 AA;
 Query Match 100.0%; Score 79; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. NO. 1.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVYDGDSDSYMN 15
 |||||
 DB 1 KASQSVYDGDSDSYMN 15
 |||||
 RESULT 10
 ABB74909
 ID ABB74909 standard; Peptide; 15 AA.
 XX AC ABB74909;
 XX 30-APR-2002 (first entry)
 XX Humanised anti-Fas antibody related peptide SEQ ID NO 26.
 XX Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;
 XX heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;
 XX autoimmune disease; allergy; atopy.
 XX OS Homo sapiens.
 XX PN JP2001342149-A.
 XX PD 11-DEC-2001.
 XX 28-MAR-2001; 2001JP-0093243.
 XX 29-MAR-2000; 2000JP-0091144.
 XX (SANY) SANKYO CO LTD.
 XX WPI; 2002-145114/19.
 XX Drug for preventing or treating e.g. autoimmune disease or allergy,
 XX comprises humanised anti-Fas antibody -
 XX Example 6 (preparatory); Page 26; 154pp; Japanese.
 XX The invention relates to a preventive or treating agent for diseases
 XX caused by abnormality in the Fas/Fas ligand system containing, as the
 XX active component, an antibody having a light chain subunit and a heavy

CC chain subunit and an activity of combining specifically with mammalian
 CC Fas and an activity of inducing apoptosis in a cell expressing Fas. The
 CC agent has antiallergic, immunosuppressive and apoptotic activity and is
 CC used for preventing and treating autoimmune diseases, allergy, atopy and
 CC others. The present sequence is that of a peptide useful to the
 CC invention.
 XX
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDYMN 15
 |||||
 Db 1 KASQSVYDGDSDYMN 15

RESULT 11
 AAR66143
 AAR66143 standard; peptide; 19 AA.

AAR66143;
 XX
 DT 12-JUL-1995 (first entry)
 XX

DE CD-4 antibody variable region complementary peptide.
 XX
 KW CD-4 antibody variable region; complementary peptide;
 KW extra-corporeal blood circulation; cell filter material.
 XX
 OS Synthetic.

XX JP06269663-A.
 XX
 PD 27-SEP-1994.
 XX

PF 17-MAR-1993; 93JP-0057206.
 PR 17-MAR-1993; 93JP-0057206.
 XX (TOYM) TOYOCO KK.
 XX

XX WPI; 1994-346316/43.
 DR

XX Material for collecting cells positive for CD-4 antibody -
 PT comprises nonwoven fabric having keto-alkyl halide functional gp
 XX

XX Example 1; Page 6; 9pp; Japanese.

CC AAR66140-R66146 are peptides complementary to the variable region
 CC of the CD-4 antibody, these peptides are fixed onto a claimed
 CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with
 CC keto-alkyl halide functional groups. This material can be used
 CC as a filter for CD-4 positive cells in a medical treatment
 CC involving the extra-corporeal circulation of blood.
 XX
 XX

SQ Sequence 19 AA;

Query Match 100.0%; Score 79; DB 15; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDYMN 15
 |||||
 Db 5 KASQSVYDGDSDYMN 19

RESULT 12
 AAY59263
 ID AAY59263 standard; protein; 103 AA.
 XX
 AC AAY59263;

XX 17-APR-2000 (first entry)
 DT
 XX Antibody 4H5 L chain variable region.
 DE
 XX CD4 antigen; anti-human; antibody; 4H5; drug.
 KW
 XX Mus sp.
 OS
 XX JPL1332563-A.
 PN
 XX 07-DEC-1999.
 PD
 XX 26-MAY-1998; 98JP-0163034.
 PF
 XX 26-MAY-1998; 98JP-0163034.
 PR
 XX (ASAH) ASAH KASEI KOGYO KK.
 PA
 XX WPI: 2000-091351/08.
 DR N-PSDB; AA258662.
 DR
 XX An antibody and the nucleic acid coding the antibody -
 PT
 PS Claim 5; Page 15-16; 25pp; Japanese.
 XX

CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the L chain variable region of the antibody 4H5.
 CC
 XX Sequence 103 AA;

Query Match 100.0%; Score 79; DB 21; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDYMN 15
 |||||
 Db 16 KASQSVYDGDSDYMN 30

RESULT 13
 AAY51140
 ID AAY51140 standard; Protein; 103 AA.
 XX
 AC AAY51140;

XX 31-MAR-2000 (first entry)
 DT
 XX Murine derived protein fragment #2.
 DE
 XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 KW
 XX Mus sp.

XX WO9961629-A1.
 PN
 XX 02-DEC-1999.
 PD
 XX 24-MAY-1999; 99WO-JP02711.
 PF
 XX 25-MAY-1998; 98JP-0159957.
 PR
 XX 26-MAY-1998; 98JP-0163023.
 PR

XX (ASAH) ASAH KASEI KOGYO KK.
 PA (ASAH) ASAH MEDICAL CO LTD.
 XX
 XX Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI: 2000-086720/07.
 DR

Fri Feb 14 15:00:54 2003

DR N-PSDB; AA444204.
XX Devices containing antibodies recognising CD4 or CD34 and their use for
PT the separation of CD4 or CD34 positive cells
XX
XX
PS Claim 22; Page 79; 11pp; Japanese.
XX
XX This invention describes a novel device (I) for separating cluster
CC differentiation (CD)-positive cells using a recombinant (chimeric or
CC single-chain) antibody recognising CD4 or CD34. The devices are useful
CC for the separation of CD4 or CD34 positive cells, which is useful for
CC the collection of hematopoietic undifferentiated cells, elimination of
CC lymphocytes from cells to be used in bone marrow transplantation, the
CC detection of leukemic cells and the production of medicinal
CC compositions for the treatment of HIV infection and autoimmune diseases.
CC This sequence represents a murine derived protein fragment which is used
CC to illustrate the method of the invention.
XX

Sequence 103 AA;
Query Match 100.0%; Score 79; DB 21; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYMN 15
DB 16 KASQSVYDGDGYMN 30

RESULT 14
AAR33309 standard; Protein: 106 AA.

XX AAR33309;
AC AAR33309;
XX 05-JUL-1993 (first entry)
XX MAE15 light chain.
XX Antibody; high affinity; FCEH; low affinity; FCEH;
KW IgE receptor; histamine; mast cell; basophil; Kabat;
KW CDR; murine; MAE11; MAE13; MAE15; MAE17.
XX Synthetic.
OS WO9304173-A.
PN 04-MAR-1993.

PF 14-AUG-1992; 92WO-US06860.
XX 14-AUG-1991; 91US-0744768.
PR 07-MAY-1992; 92US-0879495.

XX (GETH) GENENTECH INC.

XX Jardieu PM, Presta LG;

XX WPI; 1993-094004/11.

XX Polypeptide(s) binding to specific Fc epsilon receptors - act as
PT IgE antagonists; useful for treating and preventing IgE-mediated
PT disorders e.g. allergies

XX Disclosure; Fig 2; 11pp; English.

XX Antibodies capable of binding FCEH-bound IgE but which are
CC substantially incapable of binding FCEH-bound IgE or inducing
CC histamine release from mast cells or basophils, comprise a human
CC Kabat CDR domain into which has been substituted a positionally
CC analogous residue from a Kabat CDR domain of the murine anti-huIgE
CC antibodies MAE11, MAE13, MAE15 or MAE17.
XX

SQ Sequence 106 AA;

Query Match 100.0%; Score 79; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYMN 15
DB 24 KASQSVYDGDGYMN 38

RESULT 15
AAY85197 standard; protein: 106 AA.

XX AAY85197;

XX 29-JUN-2000 (first entry)

XX Light chain amino acid sequence of mouse antibody MAE15.

XX Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCEH; FCEH;
KW low affinity binding receptor; high affinity binding receptor; allergy;
KW diagnosis; treatment; histamine release; prevent; light chain.

OS Mus sp.

XX US6037453-A.

XX 14-MAR-2000.

XX 06-JUN-1995; 95US-0466151.

XX 15-MAR-1995; 95US-0405617.

XX 14-AUG-1992; 92WO-US06860.

XX 26-JAN-1994; 94US-0185899.

XX (GETH) GENENTECH INC.

XX Presta LG, Jardieu PM;

XX WPI; 2000-269913/23.

XX New bispecific antibodies, useful for treating immunoglobulin
PT E-mediated disease, binds to IgE, but only when on the low affinity
PT receptor, and to an antigen other than IgE

XX Claim 1; Fig 2; 48pp; English.

XX This sequence represents the light chain amino acid sequence of a mouse
CC anti-human immunoglobulin E (IgE) antibody. The invention relates to a
CC bispecific antibody that binds specifically to IgE when IgE is bound to
CC its low affinity receptor (FCEH), but does not bind to IgE, when IgE is
CC bound to its high affinity receptor (FCEH). The bispecific antibody
CC comprises an IgE-binding arm with human framework residues of a recipient
CC human antibody and donor murine CDR (complementarity determining region)
CC residues, but with at least one human CDR residue replacing the analogous
CC murine residue. The antibody also comprises an Fv that is specific for a
CC predetermined antigen other than IgE. The antibodies work by displacing
CC bound IgE from its receptor, or via competitive inhibition of its
CC binding. The bispecific antibodies are used for diagnosis, treatment and
CC prevention of allergy and other IgE-mediated diseases, also, when
CC immobilised, for the isolation of FCEH from cells (for research or
CC therapy). The bispecific antibodies of the invention do not cause
CC granulation or release of histamine from mast cells.
XX

SQ Sequence 106 AA;

Query Match 100.0%; Score 79; DB 21; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYMN 15

Fri Feb 14 15:00:54 2003

us-09-701-001b-4.rag

Page 8

Db 24 KASQSVYDGD SYM 38
|||||

Search completed: February 14, 2003, 11:15:44
Job time : 41.6452 secs

Fri Feb 14 15:00:54 2003

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:13:07 ; Search time 13.5484 Seconds
(without alignments)
32.575 Million cell updates/sec

Title: US-09-701-001B-4
Perfect score: 79
Sequence: 1 KASQVDYDGDGMN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA.*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	15	2	US-08-483-636-16
2	79	100.0	15	2	US-08-483-632-16
3	79	100.0	106	3	US-08-466-151-6
4	79	100.0	106	4	US-08-466-163B-6
5	79	100.0	111	1	US-08-491-845-8
6	79	100.0	111	1	US-08-491-845-16
7	79	100.0	111	2	US-08-483-636-73
8	79	100.0	111	2	US-08-483-632-73
9	79	100.0	111	2	US-08-887-352B-5
10	79	100.0	111	3	US-08-466-151-2
11	79	100.0	111	4	US-09-109-207C-5
12	79	100.0	111	4	US-08-466-163B-2
13	79	100.0	115	3	US-08-513-968-51
14	79	100.0	120	1	US-08-111-080-24
15	79	100.0	120	1	US-08-211-980-24
16	79	100.0	120	5	PCT-US93-07967-24
17	79	100.0	131	2	US-08-483-636-14
18	79	100.0	131	2	US-08-483-636-58
19	79	100.0	131	2	US-08-483-632-14
20	79	100.0	131	2	US-08-483-632-58
21	79	100.0	131	4	US-08-579-378A-14
22	79	100.0	131	4	US-08-579-378A-18
23	79	100.0	132	2	US-08-483-636-2
24	79	100.0	132	2	US-08-483-632-2
25	79	100.0	132	5	PCT-US96-13152-2
26	79	100.0	218	5	US-08-887-352B-6
27	76	96.2	111	2	US-08-483-636-16

28	76	96.2	111	4	US-09-109-207C-6	Sequence 6, Appli
29	76	96.2	111	4	US-09-296-005-6	Sequence 6, Appli
30	76	96.2	114	2	US-08-887-352B-10	Sequence 10, Appli
31	76	96.2	114	4	US-09-109-207C-10	Sequence 10, Appli
32	76	96.2	114	4	US-09-296-005-10	Sequence 10, Appli
33	76	96.2	218	2	US-08-887-352B-13	Sequence 13, Appli
34	76	96.2	218	3	US-08-466-151-9	Sequence 9, Appli
35	76	96.2	218	4	US-09-109-207C-13	Sequence 13, Appli
36	76	96.2	218	4	US-09-296-005-13	Sequence 13, Appli
37	76	96.2	218	4	US-08-466-163B-9	Sequence 9, Appli
38	73	92.4	41	3	US-08-984-277-5	Sequence 5, Appli
39	73	92.4	239	2	US-08-553-497A-18	Sequence 18, Appli
40	72	91.1	114	2	US-08-887-352B-9	Sequence 9, Appli
41	69	87.3	114	4	US-09-109-207C-9	Sequence 9, Appli
42	69	87.3	114	4	US-09-296-005-9	Sequence 9, Appli
43	53	67.1	114	2	US-08-887-352B-8	Sequence 8, Appli
44	53	67.1	218	4	US-09-282-505-1	Sequence 1, Appli
45	53	67.1	218	4	US-09-054-255-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-483-636-16
; Sequence 16, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: Intellectual Property
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-483-636-16

Query Match 100.0%; Score 79; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
| | | | | | | | | | | | | | | | |
Db 1 KASQSVYDGDGYM 15

RESULT 2

US-08-483-632-16
; Sequence 16, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-483-632-16

Query Match 100.0%; Score 79; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
| | | | | | | | | | | | | | | | |
Db 1 KASQSVYDGDGYM 15

RESULT 3

US-08-466-151-6

; Sequence 6, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

Query Match 100.0%; Score 79; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
| | | | | | | | | | | | | | | | |
Db 24 KASQSVYDGDGYM 38

RESULT 4

US-08-466-163B-6
; Sequence 6, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617

us-09-701-001b-4.rai

Fri Feb 14 15:00:54 2003

; PRIOR FILING DATE: 1995-03-15
 ; PRIOR APPLICATION NUMBER: US 08/185,899
 ; PRIOR FILING DATE: 1994-01-26
 ; PRIOR APPLICATION NUMBER: US 07/879,495
 ; PRIOR FILING DATE: 1992-05-07
 ; PRIOR APPLICATION NUMBER: US 07/744,768
 ; PRIOR FILING DATE: 1991-08-14
 ; NUMBER OF SEQ ID NOS: 64
 ; SEQ ID NO 6
 ; LENGTH: 106
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-08-466-163B-6

Query Match 100.0%; Score 79; DB 4; Length 106;
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KASQSDYDGD SYNM 15
 |||||
 24 KASQSDYDGD SYNM 38

RESULT 5
 US-08-491-845-8
 ; Sequence 8, Application US/08491845
 ; Patent No. 5773247
 ; GENERAL INFORMATION:
 ; APPLICANT: MAEDA, Hiroaki
 ; APPLICANT: KIMACHI, Kazuhiko
 ; APPLICANT: EDA, Yasuyuki
 ; APPLICANT: SHIOSAKI, Kouichi
 ; APPLICANT: OSATOMI, Kiyoshi
 ; APPLICANT: TOKIYOSHI, Sachio
 ; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
 ; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Browdy and Neimark
 ; STREET: 419 Seventh Street N.W. Ste. 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/491,845
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION NUMBER: PCT/JP93/00039
 ; FILING DATE: 14-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Browdy, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: MAEDA=5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 628-5197
 ; TELEFAX: (202) 737-3528
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 111 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-491-845-8

Query Match 100.0%; Score 79; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSDYDGD SYNM 15
 |||||
 Db 24 KASQSDYDGD SYNM 38

RESULT 6
 US-08-491-845-16
 ; Sequence 16, Application US/08491845
 ; Patent No. 5773247
 ; GENERAL INFORMATION:
 ; APPLICANT: MAEDA, Hiroaki
 ; APPLICANT: KIMACHI, Kazuhiko
 ; APPLICANT: EDA, Yasuyuki
 ; APPLICANT: SHIOSAKI, Kouichi
 ; APPLICANT: OSATOMI, Kiyoshi
 ; APPLICANT: TOKIYOSHI, Sachio
 ; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
 ; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Browdy and Neimark
 ; STREET: 419 Seventh Street N.W. Ste. 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/491,845
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION NUMBER: PCT/JP93/00039
 ; FILING DATE: 14-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Browdy, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: MAEDA=5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 628-5197
 ; TELEFAX: (202) 737-3528
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 111 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-491-845-16

Query Match 100.0%; Score 79; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSDYDGD SYNM 15
 |||||
 Db 24 KASQSDYDGD SYNM 38

RESULT 7
 US-08-483-636-73
 ; Sequence 73, Application US/08483636
 ; Patent No. 5914110
 ; GENERAL INFORMATION:
 ; APPLICANT: Holmes, Stephen D.
 ; APPLICANT: Gross, Mitchell S.
 ; APPLICANT: Sylvester, Daniel R.
 ; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in

;; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
;; NUMBER OF SEQUENCES: 75
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SmithKline Beecham Corp./Corporate
;; ADDRESSEE: Intellectual Property
;; STREET: P.O. Box 1539 / UW2220
;; CITY: King of Prussia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19406-0939
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/483,636
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/117366
;; FILING DATE: 07-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/136783
;; FILING DATE: 14-OCT-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US/94/10308
;; FILING DATE: 07-SEP-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sutton, Jeffrey A.
;; REGISTRATION NUMBER: 34,028
;; REFERENCE/DOCKET NUMBER: P50186-3
;; TELEPHONE: (215) 270-5090
;; TELEFAX: (215) 270-5090
;; INFORMATION FOR SEQ ID NO: 73:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 111 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-483-636-73

Query Match 100.0%; Score 79; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGDSDYMN 15
|||||
DB 24 KASQSVVDYDGDSDYMN 38

RESULT 8
US-08-483-632-73
;; Sequence 73, Application US/08483632
;; Patent No. 5928904
;; GENERAL INFORMATION:
;; APPLICANT: Holmes, Stephen D.
;; APPLICANT: Gross, Mitchell S.
;; APPLICANT: Sylvester, Daniel R.
;; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
;; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
;; NUMBER OF SEQUENCES: 75
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SmithKline Beecham Corp./Corporate
;; ADDRESSEE: Intellectual Property
;; STREET: P.O. Box 1539 / UW2220
;; CITY: King of Prussia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19406-0939
;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/483,632
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/117366
;; FILING DATE: 07-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/136783
;; FILING DATE: 14-OCT-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US/94/10308
;; FILING DATE: 07-SEP-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sutton, Jeffrey A.
;; REGISTRATION NUMBER: 34,028
;; REFERENCE/DOCKET NUMBER: P50186-3
;; TELEPHONE: (215) 270-5024
;; TELEFAX: (215) 270-5090
;; INFORMATION FOR SEQ ID NO: 73:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 111 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-483-632-73

Query Match 100.0%; Score 79; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGDSDYMN 15
|||||
DB 24 KASQSVVDYDGDSDYMN 38

RESULT 9
US-08-887-352B-5
;; Sequence 5, Application US/08887352B
;; Patent No. 5994511
;; GENERAL INFORMATION:
;; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
;; TITLE OF INVENTION: Improving Polypeptides
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/887,352B
;; FILING DATE: 03-Jul-1997
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Svoboda, Craig G.
;; REGISTRATION NUMBER: 39,044
;; REFERENCE/DOCKET NUMBER: P1123
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1489

us-09-701-001b-4.ra1

Fri Feb 14 15:00:54 2003

TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-5

Query Match 100.0%; Score 79; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYM 15
Db 24 KASQSVYDGDGYM 38

RESULT 10
US-08-466-151-2
Sequence 2, Application US/08466151
Patent No. 6037453

GENERAL INFORMATION:
APPLICANT: Presta, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
APPLICATION DATA: 07/879495
FILING DATE: 07-MAY-1992
APPLICATION DATA: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-466-151-2

Query Match 100.0%; Score 79; DB 3; Length 111;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYM 15
Db 24 KASQSVYDGDGYM 38

RESULT 11
US-09-109-207C-5
Sequence 5, Application US/09109207C
Patent No. 6172213

GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P112381
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 5
LENGTH: 111
TYPE: PRT
ORGANISM: Mus musculus
US-09-109-207C-5

Query Match 100.0%; Score 79; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYM 15
Db 24 KASQSVYDGDGYM 38

RESULT 12
US-09-296-005-5
Sequence 5, Application US/09296005
Patent No. 6290957

GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123C1r
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 5
LENGTH: 111
TYPE: PRT
ORGANISM: Mus musculus
US-09-296-005-5

Query Match 100.0%; Score 79; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYM 15
Db 24 KASQSVYDGDGYM 38

RESULT 13
US-08-466-163B-2
Sequence 2, Application US/08466163B
Patent No. 6329509

GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06

; PRIOR APPLICATION NUMBER: US 08/405,617
 ; PRIOR FILING DATE: 1995-03-15
 ; PRIOR APPLICATION NUMBER: US 08/185,899
 ; PRIOR FILING DATE: 1994-01-26
 ; PRIOR APPLICATION NUMBER: US 07/879,495
 ; PRIOR FILING DATE: 1992-05-07
 ; PRIOR APPLICATION NUMBER: US 07/744,768
 ; PRIOR FILING DATE: 1991-08-14
 ; NUMBER OF SEQ ID NOS: 64
 ; SEQ ID NO 2
 ; LENGTH: 111
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-08-466-163B-2

Query Match 100.0%; Score 79; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDYDGD SYNM 15
 |||||
 Db 24 KASQSDVDYDGD SYNM 38

RESULT 14
 US-08-513-968-51
 ; Sequence 51, Application US/08513968
 ; Patent No. 6114143
 ; GENERAL INFORMATION:
 ; APPLICANT: EDA, Yasuyuki
 ; APPLICANT: MAEDA, Hiroaki
 ; APPLICANT: MAKIZUMI, Keiichi
 ; APPLICANT: SHIOSAKI, Kouichi
 ; APPLICANT: OSATOMI, Kiyoshi
 ; APPLICANT: KIMACHI, Kazuhiko
 ; APPLICANT: HIGUCHI, Hirofumi
 ; APPLICANT: TOKIYOSHI, Sachio
 ; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/513,968
 ; FILING DATE: 11-SEP-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 78913/1993
 ; FILING DATE: 11-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: EDA=1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 115 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-513-968-51

Query Match 100.0%; Score 79; DB 3; Length 115;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDYDGD SYNM 15
 |||||
 Db 28 KASQSDVDYDGD SYNM 42

RESULT 15
 US-08-111-080-24
 ; Sequence 24, Application 08/111080
 ; Patent No. 5558865
 ; GENERAL INFORMATION:
 ; APPLICANT: Ohno, Tsuneya
 ; TITLE OF INVENTION: HIV Immunotherapeutics
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESSEE: Borun
 ; STREET: 6300 Sears Tower, 233 S. Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: 08/111,080
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/748,562
 ; FILING DATE: 22-AUG-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/07111
 ; FILING DATE: 24-AUG-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/039,457
 ; FILING DATE: 22-APR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Borun, Michael F.
 ; REGISTRATION NUMBER: 25,447
 ; REFERENCE/DOCKET NUMBER: 31629
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 120 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-111-080-24

Query Match 100.0%; Score 79; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDYDGD SYNM 15
 |||||
 Db 24 KASQSDVDYDGD SYNM 38

Search completed: February 14, 2003, 11:20:49
 Job time : 14.5484 secs

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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:15:53 ; Search time 8.70968 Seconds
(without alignments)
44.001 Million cell updates/sec

Title: US-09-701-001B-4

Perfect score: 79
Sequence: 1 KASQVDYDGDSTWN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications-AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	15	9	US-09-879-461-16
2	79	100.0	106	10	US-09-802-077-6
3	79	100.0	106	10	US-09-802-096-6
4	79	100.0	111	10	US-09-802-077-2
5	79	100.0	111	10	US-09-802-096-2
6	79	100.0	111	10	US-09-802-171-5
7	79	100.0	131	9	US-09-879-461-14
8	79	100.0	131	9	US-09-879-461-58
9	79	100.0	132	9	US-09-879-461-2
10	79	100.0	218	10	US-09-917-410-2
11	79	100.0	238	9	US-09-903-327A-4
12	76	96.2	111	10	US-09-920-171-6
13	76	96.2	114	10	US-09-920-171-10
14	76	96.2	218	10	US-09-802-077-9
15	76	96.2	218	10	US-09-802-096-9
16	76	96.2	218	10	US-09-920-171-13
17	69	87.3	114	10	US-09-920-171-9
18	50	63.3	114	10	US-09-920-171-8
19	50	63.3	218	10	US-09-920-171-15

20	50	63.3	218	10	US-09-920-171-17
21	50	63.3	218	10	US-09-920-171-19
22	50	63.3	218	10	US-09-920-171-24
23	50	63.3	248	10	US-09-920-171-22
24	50	63.3	248	10	US-09-920-171-23
25	46	58.2	134	10	US-09-881-823-2
26	45	57.0	111	10	US-09-920-171-7
27	42	53.2	269	12	US-10-027-770-2
28	42	53.2	269	12	US-10-027-770-5
29	41.5	52.5	222	9	US-09-479-614-26
30	41.5	52.5	242	9	US-09-479-614-20
31	41	51.9	112	9	US-09-144-886-80
32	41	51.9	112	9	US-09-144-886-81
33	41	51.9	112	9	US-09-144-886-84
34	41	51.9	112	9	US-09-144-886-85
35	41	51.9	112	9	US-09-144-886-94
36	41	51.9	112	10	US-09-810-502-36
37	41	51.9	112	10	US-09-810-502-37
38	41	51.9	172	9	US-09-854-133-111
39	41	51.9	172	10	US-09-738-973-111
40	40.5	51.3	100	10	US-09-840-459-22
41	40.5	51.3	112	9	US-10-032-482-8
42	40.5	51.3	112	10	US-09-772-120-6
43	40.5	51.3	112	10	US-09-840-459-54
44	40.5	51.3	112	10	US-09-840-459-58
45	40.5	51.3	535	9	US-09-968-851-38

ALIGNMENTS

RESULT 1

US-09-879-461-16

; Sequence 16, Application US/09879461

; Publication No. US20020193575A1

; GENERAL INFORMATION:

; APPLICANT: Holmes, Stephen D.

; Gross, Mitchell S.

; Sylvester, Daniel R.

; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in

; Treatment of IL4 Mediated Disorders

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: Corporate Intellectual Property, UW2220 - 709

; Swedeland Rd.

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406-2799

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/879,461

; FILING DATE: 12-Jun-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/612,929

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/136,783

; FILING DATE: 14-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Sutton, Jeffrey A.

; REGISTRATION NUMBER: 34,028

; REFERENCE/DOCKET NUMBER: P50186-2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 270-5024

; TELEFAX: (215) 270-5090

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-879-461-16

Query Match 100.0%; Score 79; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYN 15
| | | | | | | | | | | | | | | | | |
Db 1 KASQSVYDGDSDSYN 15

RESULT 2
US-09-802-077-6
; Sequence 6, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 6
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-6

Query Match 100.0%; Score 79; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYN 15
| | | | | | | | | | | | | | | | | |
Db 24 KASQSVYDGDSDSYN 38

RESULT 3
US-09-802-096-6
; Sequence 6, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768

;
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 6
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-6

Query Match 100.0%; Score 79; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYN 15
| | | | | | | | | | | | | | | | | |
Db 24 KASQSVYDGDSDSYN 38

RESULT 4
US-09-802-077-2
; Sequence 2, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-2

Query Match 100.0%; Score 79; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYN 15
| | | | | | | | | | | | | | | | | |
Db 24 KASQSVYDGDSDSYN 38

RESULT 5
US-09-802-096-2
; Sequence 2, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07

;; PRIOR APPLICATION NUMBER: US 07/744,768
;; PRIOR FILING DATE: 1991-08-14
;; NUMBER OF SEQ ID NOS: 64
;; SEQ ID NO 2
;; LENGTH: 111
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-802-096-2

Query Match 100.0%; Score 79; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15
Db 24 KASQSVDDYDGD SYMN 38

;; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
;; FILE REFERENCE: P1123C2US
;; CURRENT APPLICATION NUMBER: US/09/920,171
;; PRIOR FILING DATE: 2001-08-01
;; PRIOR APPLICATION NUMBER: US 08/887,352
;; PRIOR FILING DATE: 1997-07-02
;; PRIOR APPLICATION NUMBER: US 09/296,005
;; PRIOR FILING DATE: 1999-04-21
;; NUMBER OF SEQ ID NOS: 44
;; SEQ ID NO 5
;; LENGTH: 111
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-920-171-5

Query Match 100.0%; Score 79; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KASQSVDDYDGD SYMN 15
24 KASQSVDDYDGD SYMN 38

RESULT 7
US-09-879-461-14
;; Sequence 14, Application US/09879461
;; Publication No. US20020193575A1
;; GENERAL INFORMATION:
;; APPLICANT: Holmes, Stephen D.
;; Sylvester, Daniel R.
;; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
;; Treatment of IL4 Mediated Disorders
;; NUMBER OF SEQUENCES: 58
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SmithKline Beecham Corporation
;; STREET: Corporate Intellectual Property, UW2220 - 709
;; CITY: King of Prussia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19406-2799
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/879,461
;; FILING DATE: 12-Jun-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/612,929
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 08/136,783
;; FILING DATE: 14-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sutton, Jeffrey A.
;; REGISTRATION NUMBER: 34,028
;; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/879,461
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5090
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-879-461-14

Query Match 100.0%; Score 79; DB 9; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGD SYMN 15
Db 43 KASQSVDDYDGD SYMN 57

RESULT 8
US-09-879-461-58
;; Sequence 58, Application US/09879461
;; Publication No. US20020193575A1
;; GENERAL INFORMATION:
;; APPLICANT: Holmes, Stephen D.
;; Gross, Mitchell S.
;; Sylvester, Daniel R.
;; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
;; Treatment of IL4 Mediated Disorders
;; NUMBER OF SEQUENCES: 58
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SmithKline Beecham Corporation
;; STREET: Corporate Intellectual Property, UW2220 - 709
;; CITY: King of Prussia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19406-2799
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/879,461
;; FILING DATE: 12-Jun-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/612,929
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 08/136,783
;; FILING DATE: 14-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sutton, Jeffrey A.
;; REGISTRATION NUMBER: 34,028
;; REFERENCE/DOCKET NUMBER: P50186-2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-879-461-58

Query Match 100.0%; Score 79; DB 9; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
|||||

Db 43 KASQSVYDGDGYM 57
|||||

ILT 9

US-09-879-461-2
Sequence 2, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-879-461-2

Query Match 100.0%; Score 79; DB 9; Length 132;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
|||||

Db 44 KASQSVYDGDGYM 58
|||||

RESULT 10

US-09-917-410-2
Sequence 2, Application US/09917410
Patent No. US20020098183A1
GENERAL INFORMATION:
APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
CO, Man S.
TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
PREVENTION OF ACUTE ORGAN DAMAGE AFTER
EXTRACORPOREAL BLOOD CIRCULATION

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII, WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/917,410
FILING DATE: 26-Jul-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020098183A1man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: ROER 1059-PFF/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-917-410-2

Query Match 100.0%; Score 79; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
|||||

Db 24 KASQSVYDGDGYM 38
|||||

RESULT 11

US-09-903-327A-4
Sequence 4, Application US/09903327A
Patent No. US20020164333A1
GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R.
APPLICANT: Li, Erquang
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAR

;; TITLE OF INVENTION: GENE
;; TITLE OF INVENTION: DELIVERY
;; FILE REFERENCE: 22908-1228
;; CURRENT APPLICATION NUMBER: US/09/903,327A
;; CURRENT FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: 09/613,017
;; PRIOR FILING DATE: 2000-07-10
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4
;; LENGTH: 238
;; TYPE: PRT
;; ORGANISM: Mouse
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (0)...(0)
;; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
US-09-903-327A-4
Query Match 100.0%; Score 79; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 9.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDYGDSYMN 15
Db 44 KASQSVYDYGDSYMN 58
|||||

RESULT 12

US-09-920-171-6
;; Sequence 6, Application US/09920171
;; Patent No. US20020054878A1
;; GENERAL INFORMATION:
;; APPLICANT: Lowman, Henry B.
;; APPLICANT: Presta, Leonard G.
;; APPLICANT: Jardieu, Paula M.
;; APPLICANT: Lowe, John
;; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
;; CURRENT APPLICATION NUMBER: US/09/920,171
;; CURRENT FILING DATE: 2001-08-01
;; PRIOR APPLICATION NUMBER: US 08/887,352
;; PRIOR FILING DATE: 1997-07-02
;; PRIOR APPLICATION NUMBER: US 09/296,005
;; PRIOR FILING DATE: 1999-04-21
;; NUMBER OF SEQ ID NOS: 44
;; SEQ ID NO 6
;; LENGTH: 111
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: F(ab) light chain sequence derived from MAE11
US-09-920-171-6

Query Match 96.2%; Score 76; DB 10; Length 111;
Best Local Similarity 93.3%; Pred. No. 1.3e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDYGDSYMN 15
Db 24 RASQSVYDYGDSYMN 38
|||||

RESULT 13

US-09-920-171-10
;; Sequence 10, Application US/09920171
;; Patent No. US20020054878A1
;; GENERAL INFORMATION:
;; APPLICANT: Lowman, Henry B.
;; APPLICANT: Presta, Leonard G.
;; APPLICANT: Jardieu, Paula M.
;; APPLICANT: Lowe, John
;; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)

;; FILE REFERENCE: P1123C2US
;; CURRENT APPLICATION NUMBER: US/09/920,171
;; CURRENT FILING DATE: 2001-08-01
;; PRIOR APPLICATION NUMBER: US 08/887,352
;; PRIOR FILING DATE: 1997-07-02
;; PRIOR APPLICATION NUMBER: US 09/296,005
;; PRIOR FILING DATE: 1999-04-21
;; NUMBER OF SEQ ID NOS: 44
;; SEQ ID NO 10
;; LENGTH: 114
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-10

Query Match 96.2%; Score 76; DB 10; Length 114;
Best Local Similarity 93.3%; Pred. No. 1.3e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDYGDSYMN 15
Db 24 RASQSVYDYGDSYMN 38
|||||

RESULT 14

US-09-802-077-9
;; Sequence 9, Application US/09802077
;; Patent No. US20010033842A1
;; GENERAL INFORMATION:
;; APPLICANT: Presta, Leonard G.
;; APPLICANT: Jardieu, Paula M.
;; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
;; FILE REFERENCE: P0718P2C3US
;; CURRENT APPLICATION NUMBER: US/09/802,077
;; CURRENT FILING DATE: 2001-03-08
;; PRIOR APPLICATION NUMBER: US 08/405,617
;; PRIOR FILING DATE: 1995-03-15
;; PRIOR APPLICATION NUMBER: US 08/185,899
;; PRIOR FILING DATE: 1994-01-26
;; PRIOR APPLICATION NUMBER: PCT/US92/06860
;; PRIOR FILING DATE: 1992-08-14
;; PRIOR APPLICATION NUMBER: US 07/879,495
;; PRIOR FILING DATE: 1992-05-07
;; PRIOR APPLICATION NUMBER: US 07/744,768
;; PRIOR FILING DATE: 1991-08-14
;; NUMBER OF SEQ ID NOS: 64
;; SEQ ID NO 9
;; LENGTH: 218
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: humanized mae11, version 1, light chain
US-09-802-077-9

Query Match 96.2%; Score 76; DB 10; Length 218;
Best Local Similarity 93.3%; Pred. No. 2.5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDYGDSYMN 15
Db 24 RASQSVYDYGDSYMN 38
|||||

RESULT 15

US-09-802-096-9
;; Sequence 9, Application US/09802096
;; Patent No. US20010038839A1
;; GENERAL INFORMATION:
;; APPLICANT: Jardieu, Paula M.
;; APPLICANT: Presta, Leonard G.
;; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
;; FILE REFERENCE: P0718P2C3US

```

; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mael, version 1, light chain
US-09-802-096-9

```

```

Query Match          96.2%; Score 76; DB 10; Length 218;
Fast Local Similarity 93.3%; Pred No. 2.5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KASQSVYDGDSDSYMN 15
Db 24 RASQSVYDGDSDSYMN 38

```

```

Search completed: February 14, 2003, 11:21:31
Job time : 8.70968 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:12:02 ; Search time 15 Seconds
(without alignments)
96.134 Million cell updates/sec

Title: US-09-701-001b-4
Perfect score: 79
Sequence: 1 KASQSVDDYDGSYNN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	81	2 S42193	Ig kappa chain V r
2	79	100.0	93	2 A38601	Ig kappa chain V r
3	79	100.0	111	1 KVMS43	Ig kappa chain V r
4	79	100.0	111	1 KVMS83	Ig kappa chain V r
5	79	100.0	111	1 KVMS08	Ig kappa chain V r
6	79	100.0	111	1 KVMS69	Ig kappa chain V r
7	76	96.2	110	1 KVMS10	Ig kappa chain V r
8	76	96.2	112	2 PH1226	Ig kappa chain V r
9	76	96.2	131	2 S09366	Ig kappa chain pre
10	73	92.4	111	2 S09366	Ig kappa chain V-J
11	68	86.1	111	1 KVMS01	Ig kappa chain V r
12	65	82.3	112	2 S19376	Ig kappa chain V r
13	51	64.6	112	2 S19372	Ig kappa chain V r
14	48	60.8	282	2 A10948	hypothetical prote
15	46	58.2	96	2 B49442	Ig light chain V r
16	45	57.0	109	2 PH0093	Ig kappa chain V r
17	43	54.4	551	2 T03793	calmodulin-binding
18	42	53.2	102	2 PH1079	Ig light chain V r
19	42	53.2	111	1 KVMS80	Ig kappa chain V r
20	42	53.2	111	2 S09369	Ig kappa chain V-J
21	42	53.2	115	2 S63596	Ig kappa chain V r
22	42	53.2	120	2 S06732	Ig kappa chain pre
23	42	53.2	303	2 A83958	Integrase/recombin
24	41	51.9	91	2 S25462	Ig kappa chain V r
25	41	51.9	107	2 S26343	Ig kappa chain V r
26	41	51.9	107	2 S26344	Ig kappa chain V r
27	41	51.9	108	1 KVMS54	Ig kappa chain V r
28	41	51.9	111	1 KVMS37	Ig kappa chain V r
29	41	51.9	111	2 S09363	Ig kappa chain V-J

30 41 51.9 131 1 KVMSM6
31 41 51.9 340 2 E83146
32 40.5 51.3 91 2 S42186
33 40.5 51.3 101 2 A33730
34 40.5 51.3 112 2 A36259
35 40.5 51.3 113 2 F30560
36 40.5 51.3 132 2 C32513
37 40 50.6 111 2 S37202
38 40 50.6 154 1 A69012
39 40 50.6 176 2 T43335
40 40 50.6 406 2 H84590
41 40 50.6 698 2 H85633
42 40 50.6 716 1 A44259
43 40 50.6 808 2 T14513
44 39.5 50.0 83 2 S34095
45 39.5 50.0 89 2 B25155

ALIGNMENTS

RESULT 1

S42193
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S42193
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42193
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-81 <MOI>
A:Cross-references: EMBL:Z25456; NID:9407846; PIDN:CAR80943.1; PID:9407847
A:Note: the authors translated the codon GTT for residue 36 as Ala
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

Query Match 100.0%; Score 79; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGSYNN 15
|||||
DB 6 KASQSVDDYDGSYNN 20

RESULT 2

A38601
Ig kappa chain V region (IG3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: A38601
R:Goshorn, S.C.; Retzel, E.; Jemerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same anti
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: A38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-93 <GOS>
A:Cross-references: GB:M57978; NID:g196402; PIDN:AAA63359.1; PID:g196403
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

Query Match 100.0%; Score 79; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGSYNN 15
|||||

Db 5 KASQSVYDGDSDSYMN 19

RESULT 3

KVMS43

Ig kappa chain V region (PC7043) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000

C:Accession: A01937; S42187; S42194; S42189; S42188; S42191; S42192

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: A01937

A:Molecule type: protein

A:Residues: 1-111 <WEI>

R:Mo, J.A.; Bona, C.A.; Holmdahl, R.

Eur. J. Immunol. 23, 2503-2510, 1993

A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec

A:Reference number: S42176; MUID:94009207; PMID:7691608

A:Accession: S42187

A:Molecule type: DNA

A:Residues: 10-99 <MOJ>

A:Cross-references: EMBL:Z25444; NID:9407832; PIDN:CAA80931.1; PID:9407833

A:Note: V-kappa-21E; anti-collagen

A:Accession: S42194

A:Molecule type: DNA

A:Residues: 12-99 <MOV>

A:Cross-references: EMBL:Z25458; NID:9407844; PIDN:CAA80945.1; PID:9407845

A:Note: V-kappa-21E; anti-collagen

A:Accession: S42190

A:Molecule type: DNA

A:Residues: 13-99 <MOF>

A:Cross-references: EMBL:Z25450; NID:9407838; PIDN:CAA80937.1; PID:9407839

A:Note: V-kappa-21E; anti-collagen

A:Accession: S42189

A:Molecule type: DNA

A:Residues: 15-99 <MOA>

A:Cross-references: EMBL:Z25448; NID:9407836; PIDN:CAA80935.1; PID:9407837

A:Note: V-kappa-21E; anti-collagen

A:Accession: S42188

A:Molecule type: DNA

A:Residues: 12-99 <MOY>

A:Cross-references: EMBL:Z25446; NID:9407834; PIDN:CAA80933.1; PID:9407835

A:Note: V-kappa-21E; anti-collagen

A:Accession: S42191

A:Molecule type: DNA

A:Residues: 10-99 <MOY>

A:Cross-references: EMBL:Z25452; NID:9407840; PIDN:CAA80939.1; PID:9407841

A:Note: V-kappa-21E; anti-collagen

A:Accession: S42192

A:Molecule type: DNA

A:Residues: 10-99 <MOO>

A:Cross-references: EMBL:Z25454; NID:9407842; PIDN:CAA80941.1; PID:9407843

A:Note: V-kappa-21E; anti-collagen

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 79; DB 1; Length 111;

Best Local Similarity 100.0%; Pred. No. 4.5e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDSDSYMN 15

Db 24 KASQSVYDGDSDSYMN 38

RESULT 4

KVMS83

Ig kappa chain V region (PC7183) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000

C:Accession: B01937; A01937

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: B01937

A:Molecule type: protein

A:Residues: 1-111 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 79; DB 1; Length 111;

Best Local Similarity 100.0%; Pred. No. 4.5e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDSDSYMN 15

Db 24 KASQSVYDGDSDSYMN 38

RESULT 5

KVMS08

Ig kappa chain V region (PC6308) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000

C:Accession: C01937; A01937

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: C01937

A:Molecule type: protein

A:Residues: 1-111 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 79; DB 1; Length 111;

Best Local Similarity 100.0%; Pred. No. 4.5e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDSDSYMN 15

Db 24 KASQSVYDGDSDSYMN 38

RESULT 6

KVMS69

Ig kappa chain V region (PC7769) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000

C:Accession: E01937; A01937

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: E01937

A:Molecule type: protein

A:Residues: 1-111 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 86.1%; Score 68; DB 1; Length 111;
 Best Local Similarity 86.7%; Pred. No. 0.00031;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15
 ||||| |||||
 DB 24 KASQSVDTGESYMN 38

RESULT 12

S19976

Ig kappa chain V region (M-T413) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

Accession: S19976

Geissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

Submitted to the EMBL Data Library, March 1992

A;Description: Structural characterization of CD4 mAb.

A;Reference number: S19963

A;Accession: S19976

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-112 <WEI>

A;Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID:g52299

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 65; DB 2; Length 112;
 Best Local Similarity 80.0%; Pred. No. 0.001;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15
 ||||| |||||
 DB 24 KASQSLDYDADSYMH 38

RESULT 13

S19972

Ig kappa chain V region (M-T321) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

Accession: S19972

Geissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

Submitted to the EMBL Data Library, March 1992

A;Description: Structural characterization of CD4 mAb.

A;Reference number: S19963

A;Accession: S19972

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-112 <WEI>

A;Cross-references: EMBL:X65094; NID:g52290; PIDN:CAA46222.1; PID:g52291

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 64.6%; Score 51; DB 2; Length 112;
 Best Local Similarity 66.7%; Pred. No. 0.22;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15
 ||||| |||||
 DB 24 KASQSVDYNAISYMH 38

RESULT 14

AI0948

hypothetical protein STY3863 [imported] - Salmonella enterica subsp. enterica serovar
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
 C;Accession: AI0948
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
 th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
 S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se

A;Reference number: AB0502; PMID:11677608

A;Accession: AI0948

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-282 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD09611.1; PID:g16504722; GSPDB:GN00176

C;Genetics:

A;Gene: STY3863

Query Match 60.8%; Score 48; DB 2; Length 282;
 Best Local Similarity 60.0%; Pred. No. 1.8;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15
 :| : ||||| |||
 DB 263 EALEPDDYDGD SYMN 277

RESULT 15

B49442

Ig light chain V region (50.1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C;Accession: B49442

R;Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapié, L.M.

Proteins 14, 499-508, 1992

A;Title: Crystallization, sequence, and preliminary crystallographic data for an anti

A;Reference number: A49442; MUID:93066166; PMID:1438187

A;Accession: B49442

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-96 <STU>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F:8-86/Domain: immunoglobulin homology <IMM>

Query Match 58.2%; Score 46; DB 2; Length 96;
 Best Local Similarity 53.3%; Pred. No. 1.3;
 Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15
 :||: ||| |||: |||
 DB 16 RASESVDDGNSFLH 30

Search completed: February 14, 2003, 11:19:47
 Job time : 16 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:05:27 ; Search time 7.74194 Seconds
(without alignments)
80.360 Million cell updates/sec

Title: US-09-701-001b-4
Perfect score: 79
Sequence: 1 KASQSDVDGDSYMN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	111	1 KV3M_MOUSE	P01665 mus musculus
2	79	100.0	111	1 KV3N_MOUSE	P01666 mus musculus
3	79	100.0	111	1 KV3Q_MOUSE	P01667 mus musculus
4	79	100.0	111	1 KV3O_MOUSE	P01668 mus musculus
5	76	96.2	110	1 KV3P_MOUSE	P01669 mus musculus
6	68	86.1	111	1 KV3L_MOUSE	P01670 mus musculus
7	45	57.0	111	1 KV3C_MOUSE	P01671 mus musculus
8	43	54.4	682	1 KIF2_XENLA	P01672 xenopus lae
9	42	53.2	111	1 KV3A_MOUSE	P01673 mus musculus
10	42	53.2	112	1 KV3B_MOUSE	P01674 mus musculus
11	41	51.9	108	1 KV3V_MOUSE	P01675 mus musculus
12	41	51.9	111	1 KV3H_MOUSE	P01676 mus musculus
13	41	51.9	111	1 KV3J_MOUSE	P01677 mus musculus
14	41	51.9	111	1 KV3K_MOUSE	P01678 mus musculus
15	41	51.9	131	1 KV3I_MOUSE	P01679 mus musculus
16	41	51.9	459	1 CCMH_HAEIN	P46458 haemophilus
17	40	50.6	112	1 KV3G_MOUSE	P01680 mus musculus
18	40	50.6	171	1 ALL8_OLEEU	Q9m710 olea europae
19	40	50.6	679	1 KIF2_HUMAN	O00139 homo sapien
20	40	50.6	716	1 KIF2_MOUSE	P28740 mus musculus
21	39.5	50.0	133	1 KV2F_HUMAN	P06310 homo sapien
22	39	49.4	334	1 VE2_BPV4	P08345 bovine papi
23	39	49.4	409	1 TH1L_PANTH	P45741 paenibacill
24	39	49.4	638	1 PDA4_MOUSE	P08003 mus musculus
25	39	49.4	643	1 PDA4_RAT	P38659 rattus norv
26	38.5	48.7	75	1 LSM6_SCHPO	Q9uull schizosacch
27	38	48.1	83	1 TBB3_SOYBN	P01064 glycine max
28	38	48.1	123	1 YF31_CAEEL	Q93196 caenorhabdi
29	38	48.1	230	1 DAG_ANTWA	Q38732 antirrhinum
30	38	48.1	243	1 LPSB_LYTP1	Q03975 lytechinus
31	38	48.1	260	1 CABV_BOVIN	P04467 bos taurus
32	38	48.1	272	1 TYPH_MYCHO	P43050 mycoplasma
33	38	48.1	315	1 CALU_HUMAN	O43852 homo sapien

34	38	48.1	321	1 LPSA_LYTP1	P09485 lytechinus
35	38	48.1	369	1 VE2_HPV66	Q80958 human papil
36	38	48.1	407	1 YK85_CAEEL	P34311 caenorhabdi
37	38	48.1	512	1 VC02_VACCC	P21037 vaccinia vi
38	38	48.1	512	1 VC02_VACCV	P17371 vaccinia vi
39	38	48.1	823	1 YN52_CAEEL	P34586 caenorhabdi
40	38	48.1	1173	1 YN52_XENLA	P35448 xenopus lae
41	38	48.1	1592	1 YHD5_YEAST	P38735 saccharomyc
42	37.5	47.5	80	1 LSM6_HUMAN	Q9Y4V8 homo sapien
43	37.5	47.5	113	1 KV2B_HUMAN	P01615 homo sapien
44	37.5	47.5	350	1 Y4RM_HUISN	P55646 rhizobium s
45	37	46.8	80	1 YV6A_VIBCH	P58093 vibrio chol

ALIGNMENTS

RESULT 1					
KV3M_MOUSE					
ID	KV3M_MOUSE	STANDARD;	PRT;	111 AA.	
AC	P01665;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V-III region PC 7043.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=79073152; PubMed=103003;				
RA	Weigert M., Gatmaian L., Loh E., Schilling J., Hood L.E.;				
RT	"Rearrangement of genetic information may produce immunoglobulin				
RT	diversity."				
RL	Nature 276:785-790(1978).				
DR	PIR; A01937; KVM543.				
DR	HSSP; P80362; IWT.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; IGV; 1.				
DR	Immunoglobulin V region.				
KW	DOMAIN 1 23				
FT	DOMAIN 24 38				FRAMEWORK-1.
FT	DOMAIN 39 53				COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 54 60				FRAMEWORK-2.
FT	DOMAIN 61 92				COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 93 101				FRAMEWORK-3.
FT	DOMAIN 102 111				COMPLEMENTARITY-DETERMINING-3.
FT	DISULFID 23 92				FRAMEWORK-4.
FT	NON_TER 111 111				BY SIMILARITY.
SQ	SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;				

Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.le-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSDVDGDSYMN 15

Db 24 KASQSDVDGDSYMN 38

RESULT 2

KV3N_MOUSE					
ID	KV3N_MOUSE	STANDARD;	PRT;	111 AA.	
AC	P01666;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V-III region PC 7183.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				

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OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR HSP; P01679; KVM583.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.le-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
DB 24 KASQSVYDGDGYM 38
|||||

RESULT 3
KV30_MOUSE STANDARD; PRT; 111 AA.
ID KV30_MOUSE
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 5308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR HSP; P80362; LWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.le-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
DB 24 KASQSVYDGDGYM 38
|||||

RESULT 4
KV30_MOUSE STANDARD; PRT; 111 AA.
ID KV30_MOUSE
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR HSP; P80362; LWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.le-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
DB 24 KASQSVYDGDGYM 38
|||||

RESULT 5
KV3P_MOUSE STANDARD; PRT; 110 AA.
ID KV3P_MOUSE
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";

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Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.le-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
DB 24 KASQSVYDGDGYM 38
|||||

RESULT 4
KV3Q_MOUSE STANDARD; PRT; 111 AA.
ID KV3Q_MOUSE
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR HSP; P80362; LWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.le-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
DB 24 KASQSVYDGDGYM 38
|||||

RESULT 5
KV3P_MOUSE STANDARD; PRT; 110 AA.
ID KV3P_MOUSE
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";

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RL Nature 276:785-790(1978).
DR PIR: D01937; KVM510.
DR HSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 100
FT DOMAIN 101 110
FT DOMAIN 111 120
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 96.2%; Score 76; DB 1; Length 110;
Best Local Similarity 93.3%; Pred. No. 3.5e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSDYDGDGYM 15
Db 24 KASQSLDYDGDGYM 38

RESULT 6
KV3L_MOUSE STANDARD; PRT; 111 AA.
ID KV3L_MOUSE
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
PIR: A01936; KVM5C1.
DR HSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2BIAD98AD965962 CRC64;

Query Match 86.1%; Score 68; DB 1; Length 111;
Best Local Similarity 86.7%; Pred. No. 8.1e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 KASQSDYDGDGYM 15
Db 24 KASQSLDYDGDGYM 38

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RESULT 7
KV3C_MOUSE STANDARD; PRT; 111 AA.
ID KV3C_MOUSE
AC P01656;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 70.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=67056897; PubMed=4162931;
RA Gray W.R., Dreyer W.J., Hood L.E.;
RT "Mechanism of antibody synthesis: size differences between mouse
kappa chains.";
Science 155:465-467(1967).
-!- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
PIR: A01930; KVM580.
DR HSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Bence-Jones protein.
KW DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11904 MW; 4FE7ABC9DF0FC125 CRC64;

Query Match 57.0%; Score 45; DB 1; Length 111;
Best Local Similarity 60.0%; Pred. No. 0.66;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KASQSDYDGDGYM 15
Db 24 RASEVDNSGISEPMN 38

RESULT 8
KIF2_XENLA STANDARD; PRT; 682 AA.
ID KIF2_XENLA
AC Q91637;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kinesin-like protein KIF2 (Kinesin-related protein XKIF2).
KW KIF2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A., AND REVISIONS.
RX Walczak C.E.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN RP SEQUENCE OF 124-682 FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE=96140638; PubMed=8548824;
RA Walczak C.E., Mitchelson T.J., Desai A.;

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RT "XKCM1: a Xenopus kinesin-related protein that regulates microtubule
 RL dynamics during mitotic spindle assembly.";
 CC Cell 84:37-47(1996).
 CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. MCAK/KIF2
 CC SUBFAMILY.
 CC -----
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 CC -----

DR EMBL; U36486; AAC59744.2; ALT_INIT.
 DR HSPSP; P17119; 3KAR.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; kinesin_1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
 DR Motor protein; Microtubules; ATP-binding; Coiled coil.
 DR DOMAIN 1 192 GLOBULAR (POTENTIAL)
 FT DOMAIN 193 542 KINESIN_MOTOR (BY SIMILARITY).
 FT DOMAIN 543 682 COILED COIL (POTENTIAL).
 FT NP_BIND 288 295 ATP (BY SIMILARITY).
 SQ SEQUENCE 682 AA; 77414 MW; 3DA295B319063F8 CRC64;

Query Match 54.4%; Score 43; DB 1; Length 682;
 Best Local Similarity 63.6%; Pred. No. 11;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 SQSVVDYDGSY 13
 Db :: ||||| |||
 625 TEEVDYDADSY 635

RESULT 9
 KV3A_MOUSE STANDARD; PRT; 111 AA.
 ID KV3A_MOUSE
 AC P01654;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 2880/PC 1229.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCB1_TaxID=10090;
 [1]
 SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 CC -!- MISCELLANEOUS: THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL.
 DR PIR; A01930; KVM580.
 DR HSPSP; P80362; 1WTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 102
 FT DOMAIN 103 111
 FT DISULFID 102 111
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12054 MW; 5F0DD25EE20BE611 CRC64;
 Query Match 53.2%; Score 42; DB 1; Length 112;
 Best Local Similarity 60.0%; Pred. No. 2.2;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

FT NON_TER 111
 SQ SEQUENCE 111 AA; 11980 MW; AFEAC6A9D26FC12D CRC64;
 Query Match 53.2%; Score 42; DB 1; Length 111;
 Best Local Similarity 60.0%; Pred. No. 2.2;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

RESULT 10

KV3B_MOUSE STANDARD; PRT; 112 AA.
 ID KV3B_MOUSE
 AC P01655;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 7132.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCB1_TaxID=10090;
 [1]
 SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 CC -!- MISCELLANEOUS: THE PC 7132 AND PC 1229 SEQUENCES ARE IDENTICAL.
 DR PIR; A01930; KVM580.
 DR HSPSP; P01679; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 102
 FT DOMAIN 103 112
 FT DISULFID 23 92
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 12054 MW; 5F0DD25EE20BE611 CRC64;
 Query Match 53.2%; Score 42; DB 1; Length 112;
 Best Local Similarity 60.0%; Pred. No. 2.2;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGSYMN 15
 Db ::||| ||| |||
 24 RASESDVNYGISFMN 38

RESULT 11
 KV3V_MOUSE STANDARD; PRT; 108 AA.
 ID KV3V_MOUSE
 AC P01674;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 2154.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCB1_TaxID=10090;
 [1]
 SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;

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RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity";
RL Nature 276:785-790(1978).
DR PIR: A01940; KVM54.
DR HSP: P80362; IWLTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 108
FT DISULFID 23 92
FT NON_TER 108 108
SQ SEQUENCE 108 AA; D40921D18DAC4B9E CRC64;

Query Match 51.9%; Score 41; DB 1; Length 108;
Best Local Similarity 60.0%; Pred. No. 3.1;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMN 15
:||||| :|:|:
Db 24 RASQSVSTGSGSYMH 38

RESULT 12
KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity";
RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79073152; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -1- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR: A01934; KVM537.
DR HSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
FT SEQUENCE 111 AA; D7DF0609303453CE CRC64;

Query Match 51.9%; Score 41; DB 1; Length 111;
Best Local Similarity 53.3%; Pred. No. 3.2;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMN 15
:||||| :|:|:
Db 24 RASQSVSTGSGSYMH 38

RESULT 14
KV3K_MOUSE STANDARD; PRT; 111 AA.
ID KV3K_MOUSE
AC P01663;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

FT NON_TER 111
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;
Query Match 51.9%; Score 41; DB 1; Length 111;
Best Local Similarity 53.3%; Pred. No. 3.2;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMN 15
:||||| :|:|:
Db 24 RASQSVSTGSGSYMH 38

RESULT 13
KV3J_MOUSE STANDARD; PRT; 111 AA.
ID KV3J_MOUSE
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity";
RL Nature 276:785-790(1978).
CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR: A01935; KVM56.
DR HSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
FT SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 51.9%; Score 41; DB 1; Length 111;
Best Local Similarity 53.3%; Pred. No. 3.2;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMN 15
:||||| :|:|:
Db 24 RASQSVSTGSGSYMH 38

RESULT 14
KV3K_MOUSE STANDARD; PRT; 111 AA.
ID KV3K_MOUSE
AC P01663;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

```

DE Ig kappa chain V-III region PC 4050.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; A01935; KVM5M6.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT CHAIN 1 20
FT SIGNAL 1 20
FT DOMAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 73 FRAMEWORK-2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 81 112 FRAMEWORK-3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 131 FRAMEWORK-4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match 51.9%; Score 41; DB 1; Length 111;
Best Local Similarity 53.3%; Pred. NO. 3.2;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYMN 15
Db 24 RASESDVSYGNSFMH 38
:||||| i:|:|:

RESULT 15
KV31_MOUSE
ID KV31_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";

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Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
PIR; A01935; KVM5M6.
HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT SIGNAL 1 20
FT DOMAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 73 FRAMEWORK-2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 81 112 FRAMEWORK-3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 131 FRAMEWORK-4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 51.9%; Score 41; DB 1; Length 131;
Best Local Similarity 53.3%; Pred. NO. 3.8;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYMN 15
Db 44 RASESDVSYGNSFMH 58
:||||| i:|:|:

Search completed: February 14, 2003, 11:16:22
Job time : 8.74194 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:10:17 ; Search time 31.2097 Seconds
(without alignments)
99.030 Million cell updates/sec

Title: US-09-701-001B-4
Perfect score: 79
Sequence: 1 KASQSVYDGD SYMN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organalle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-rvivirus:*
16: sp-bacteriap:*
17: sp-archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	48	60.8	282	16 Q8ZKU0	Q8ZKU0 salmonella
2	48	60.8	282	16 Q8ZS9	Q8ZS9 salmonella
3	44	55.7	542	5 Q9NJD9	Q9NJD9 onchocerca
4	44	55.7	815	3 Q9C107	Q9C107 schizosacch
5	43	54.4	137	11 P97596	P97596 rattus norv
6	43	54.4	186	5 Q9W2L0	Q9W2L0 drosophila
7	43	54.4	551	10 P93370	P93370 nicotiana t
8	43	54.4	1868	10 Q9LVX3	Q9LVX3 arabidopsis
9	42	53.2	153	10 Q9AQY5	Q9AQY5 polytomella
10	42	53.2	218	11 Q9Z5S1	Q9Z5S1 mus musculu
11	42	53.2	303	16 Q9KA25	Q9KA25 bacillus ha
12	41	51.9	168	11 Q9JI46	Q9JI46 mus musculu
13	41	51.9	172	4 Q95989	Q95989 homo sapien
14	41	51.9	336	2 Q9X6V5	Q9X6V5 pseudomonas
15	41	51.9	340	16 Q9HX24	Q9HX24 pseudomonas
16	40	50.6	131	10 Q9SRP5	Q9SRP5 arabidopsis

17	40	50.6	137	10 Q9SRP4	Q9SRP4 arabidopsis
18	40	50.6	154	17 Q27163	Q27163 methanobact
19	40	50.6	176	3 Q42711	Q42711 schizosacch
20	40	50.6	180	11 Q9D058	Q9D058 mus musculu
21	40	50.6	197	16 Q92L50	Q92L50 thizobium m
22	40	50.6	247	11 Q9WV63	Q9WV63 rattus norv
23	40	50.6	311	2 Q86071	Q86071 pseudomonas
24	40	50.6	420	10 Q9SIV3	Q9SIV3 arabidopsis
25	40	50.6	609	4 Q9H2V9	Q9H2V9 homo sapien
26	40	50.6	610	11 Q9D6X1	Q9D6X1 mus musculu
27	40	50.6	610	11 Q99KW9	Q99KW9 mus musculu
28	40	50.6	610	11 Q8R4E1	Q8R4E1 rattus norv
29	40	50.6	612	4 Q8TB96	Q8TB96 homo sapien
30	40	50.6	615	4 Q9BRE2	Q9BRE2 homo sapien
31	40	50.6	659	11 Q54744	Q54744 mus musculu
32	40	50.6	678	11 Q91W03	Q91W03 mus musculu
33	40	50.6	808	10 Q9SW62	Q9SW62 arabidopsis
34	40	50.6	921	10 Q9FH44	Q9FH44 arabidopsis
35	40	50.6	984	12 Q8QS29	Q8QS29 chimpanzee
36	40	50.6	2439	5 Q9VMS2	Q9VMS2 drosophila
37	39	49.4	103	11 Q9JL80	Q9JL80 mus musculu
38	39	49.4	196	9 Q94MM9	Q94MM9 cyanophage
39	39	49.4	200	2 Q9AER3	Q9AER3 serratia ma
40	39	49.4	262	5 Q05432	Q05432 bombyx mori
41	39	49.4	276	17 Q9HRR1	Q9HRR1 halobacteri
42	39	49.4	349	10 Q9FNE9	Q9FNE9 arabidopsis
43	39	49.4	445	2 Q9AMT8	Q9AMT8 bradyrhizob
44	39	49.4	508	5 Q9NA84	Q9NA84 caenorhabdi
45	39	49.4	509	5 Q27482	Q27482 caenorhabdi

ALIGNMENTS

RESULT 1

ID	Q8ZKU0	PRELIMINARY;	PRT;	282 AA.
AC	Q8ZKU0;			
DT	01-MAR-2002 (TREMREL. 20, Created)			
DT	01-MAR-2002 (TREMREL. 20, Last sequence update)			
DT	01-MAR-2002 (TREMREL. 20, Last annotation update)			
DE	Putative cytoplasmic protein.			
GN	STM4015.			
OS	Salmonella typhimurium.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Salmonella.			
OX	NCBI_TaxID=602;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=LT2 / SCSC1412 / ATCC 700720;			
RX	MEDLINE=21534948; PubMed=11677609;			
RA	McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,			
RA	Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,			
RA	Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,			
RA	Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,			
RA	Waterston R., Wilson R.K.;			
RT	*Complete genome sequence of Salmonella enterica serovar Typhimurium			
RT	LT2.;			
RL	Nature 413:852-856(2001).			
DR	EMBL: AE008887; AAL22854.1; .			
KW	Hypothetical protein; Complete proteome.			
SQ	SEQUENCE 282 AA; 31896 MW; 192CAAE31679D2C6 CRC64;			

Query Match 60.8%; Score 48; DB 16; Length 282;
Best Local Similarity 60.0%; Pred. No. 3.1;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KASQSVYDGD SYMN 15

Db 263 EALEPDDYDGD IYMN 277

RESULT 2

```

Q822S9
ID Q822S9 PRELIMINARY; PRT; 282 AA.
AC Q822S9;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Hypothetical protein STY3863.
GN STY3863.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OC NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leath A.S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar typhi CT18."
RL Nature 413:848-852(2001).
DR EMBL; AL627279; CAP09611.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 282 AA; 31930 MW; EBCB0B08D8D6E877 CRC64;

Query Match 60.8%; Score 48; DB 16; Length 282;
Best Local Similarity 60.0%; Pred. No. 3.1;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQVDYDGDYSYN 15
Db 263 EALEPDDYDGDYIN 277
I:| | | | | | | |

RESULT 3
Q9NJD9 PRELIMINARY; PRT; 542 AA.
ID Q9NJD9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Calcium-binding protein CBP-1.
GN CBP-1.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20278137; PubMed=10816503;
RA Lizotte-Waniewski M., Tawe W., Gulliano D.B., Lu W., Liu J.,
RA Williams S.A., Lustigman S.;
RT "Identification of potential vaccine and drug target candidates by
RT expressed sequence tag analysis and immunoscreening of Onchocerca
RT volvulus larval cDNA libraries."
RL Infect. Immun. 68:3491-3501(2000).
DR EMBL; AF153720; AAF64251.1; -.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 10.
DR SMART; SM00054; EFh; 8.
DR PROSITE; PS00018; EF_HAND;
SQ SEQUENCE 542 AA; 61269 MW; 94E3D57FB72D805B CRC64;

Query Match 55.7%; Score 44; DB 5; Length 542;
Best Local Similarity 58.3%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY 4 QSDYDGDYSYN 15
Db 380 QEIDSDGDYIN 391
I:| | | | | | | |

RESULT 4
Q9CL07 PRELIMINARY; PRT; 815 AA.
ID Q9CL07;
AC Q9CL07;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 91.0 kDa protein.
GN SPAPBIE7.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Wood V., Rajandream M.A., Barrell B.G., Seeger K., Harris D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AL590605; CAC36919.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 6.
DR SMART; SM00320; WD40; 6.
DR PROSITE; PS00082; WD_REPEATS_2; 1.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 815 AA; 90985 MW; D3AD3EF2D7997C54 CRC64;

Query Match 55.7%; Score 44; DB 3; Length 815;
Best Local Similarity 80.0%; Pred. No. 52;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SVDYDGDYSYN 14
Db 366 SLDLDGDYSYN 375
I:| | | | | | | |

RESULT 5
P97596 PRELIMINARY; PRT; 137 AA.
ID P97596;
AC P97596;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Mast cell protease 10 (Fragment).
GN MCP-10.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RX MEDLINE=97149430; PubMed=8996238;
RA Lutzeischwab C., Pejler G., Aveskogh M., Hellman L.;
RT "Secretory granule proteases in rat mast cells. Cloning of 10
RT different serine proteases and a carboxypeptidase A from various rat
RT mast cell populations."
RL J. Exp. Med. 185:13-29(1997).
DR EMBL; U67913; AAB48266.1; -.
DR HSP; P04187; 2CPI.
DR MEROPS; S01.008; -.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00020; Tryp-SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
KW Hydrolase; Protease; Serine protease.

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FT NON_TER 1 1
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15019 MW; 83632B52786085BF CRC64;

Query Match 54.4%; Score 43; DB 11; Length 137;
Best Local Similarity 53.3%; Pred. No. 10;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYM 15
DB 29 KAKPHENYDGDSDHFN 43
||:|||||:|

RESULT 6
Q9W2L0 PRELIMINARY; PRT; 186 AA.
AC Q9W2L0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CG9406 protein.
GN CG9406.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Abayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou W., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003453; AA46680.1;
DR HSP; F02588; 1F0N.
DR FlyBase; FBgn0034592; CG9406.
DR InterPro; IPR002048; EF-hand.

DR Pfam: PF00036; efhand; 2.
DR ProDom: PD000012; EP-hand; 1.
SQ SEQUENCE 186 AA; 21301 MW; 7B8A6AA5A87AFAFE CRC64;

Query Match 54.4%; Score 43; DB 5; Length 186;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYM 14
DB 56 KATSDVDYDGEAHL 69
||:|||||:|

RESULT 7
P93370 PRELIMINARY; PRT; 551 AA.
ID P93370;
AC P93370;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Calmodulin-binding protein.
GN TCB60.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISCONSIN 38;
RT Dash S., Lu Y., Harrington H.M.;
RT "Molecular cloning and characterization of a tobacco calmodulin-
RT binding protein.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U58971; AAB37246.1;
SQ SEQUENCE 551 AA; 61598 MW; 813879E25125C374 CRC64;

Query Match 54.4%; Score 43; DB 10; Length 551;
Best Local Similarity 53.8%; Pred. No. 49;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 SQSDVDYDGDSDYM 15
DB 292 NQVVEYDGRKFLN 304
||:|||||:|

RESULT 8
Q9LVX3 PRELIMINARY; PRT; 1868 AA.
ID Q9LVX3;
AC Q9LVX3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Genomic DNA, chromosome 3, pl clone; MGF10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty pl and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).

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DR EMBL; AB018114; BAB02691.1; -.
DR InterPro; IPR001395; ALDO/ket_red.
DR PROSITE; PS000345; CYC_heme_bind.
DR PROSITE; PS00063; ALDO_KETO_REDUCTASE_3; UNKNOWN_1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SQ SEQUENCE 1868 AA; 206712 MW; 0799ADC38CC0C5F0 CRC64;

Query Match          54.4%; Score 43; DB 10; Length 1868;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYN 15
Db 1074 EASASDSDSDSYN 1088
      :|||:|:|:|:|:|
      :|||:|:|:|:|:|

RESULT 9
ID Q9A0Y5 PRELIMINARY; PRT; 153 AA.
AC Q9A0Y5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytochrome C oxidase polypeptide II (EC 1.9.3.1).
GN COX2B.
OS Polytomella sp. 'Pringsheim 198.80'.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Polytomella.
OX NCBI_TaxID=37502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRINGSHEIM 198.80;
RX PubMed=11094061;
RA Perez-Martinez X., Antaramian A., Vazquez-Acevedo M., Funes S.,
RA Tolkunova E., d'Alayer J., Claros M.G., Davidson E., King M.P.,
RA Gonzalez-Halphen D.;
RT "Subunit II of Cytochrome C Oxidase in Chlamydomonas Algae Is a
RT Heterodimer Encoded by Two Independent Nuclear Genes.";
RL J. Biol. Chem. 276:11302-11309(2001).
CC 1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. SUBUNIT 2
CC TRANSFERS THE ELECTRONS FROM CYTOCHROME C VIA ITS BINUCLEAR COPPER
CC A CENTER TO THE BIMETALLIC CENTER OF THE CATALYTIC SUBUNIT 1 (BY
CC SIMILARITY).
CC 1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICCYTOCHROME
CC C + 2 H(2)O.
CC 1- COFACTOR: COPPER A AND HEME GROUP (BY SIMILARITY).
CC 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.
EMBL; AF305542; AAK32116.1; -.
DR EMBL; AF305079; AAK30366.1; -.
DR HSSP; P18400; ICYX.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR002429; Cyt_c_ox_2.
DR Pfam; PF00116; COX2; 1.
DR PRINTS; PR01166; CYCOXIDASEII.
DR ProDom; PD000131; Copper_CuA; 1.
DR PROSITE; PS00078; COX2; 1.
KW Copper; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
SQ SEQUENCE 153 AA; 17219 MW; A69030F3E4746238 CRC64;

Query Match          53.2%; Score 42; DB 10; Length 153;
Best Local Similarity 61.5%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ASQSVYDGDSDSYN 14
Db 36 ASQPIQYDFDSYN 48
      |||:|:|:|:|
      |||:|:|:|:|

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RESULT 10
Q925S1 PRELIMINARY; PRT; 218 AA.
ID Q925S1
AC Q925S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
FT NON_TER 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match          53.2%; Score 42; DB 11; Length 218;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYN 15
Db 159 RASESVDNIGISFMN 173
      :|||:|:|:|:|
      :|||:|:|:|:|

RESULT 11
Q9KA25 PRELIMINARY; PRT; 303 AA.
ID Q9KA25
AC Q9KA25;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Integrase/recombinase.
GN CODY OR BH2465.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirano C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001515; BAB06184.1; -.
DR HSSP; P21891; LAOP.
DR InterPro; IPR002104; Phage_integrase.
DR InterPro; IPR004107; Phage_integr_N.
DR Pfam; PF00589; Phage_integrase; 1.
DR Pfam; PF02899; Phage_integr_N; 1.

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KW Complete proteome. 35035 MW; D10E8AAAEFD6705 CRC64;
 SQ SEQUENCE 303 AA; 53.2%; Score 42; DB 16; Length 303;
 Query Match 53.3%; Pred. No. 37;
 Best Local Similarity 53.3%;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDY 15
 DB 204 KKSQVDLPDGLN 218
 ID Q9J146 PRELIMINARY; PRT; 168 AA.
 AC Q9J146; PRELIMINARY; PRT; 168 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Diphosphoinositol polyphosphate phosphohydrolase (Nudix (nucleotide
 DE diphosphate linked moiety X)-type motif 3).
 GN NUDT3 OR DRPP.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RA Chu C., Timo K., Lisanti M., Burstein D., Kohtz D.;
 RA "Ectopic Expression of Diphosphoinositol Polyphosphate
 RA Phosphohydrolase (dIPP).";
 RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RL SEQUENCE FROM N.A.
 RP Strausberg R.;
 RP Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF264064; AAF74761.1; -
 DR EMBL; BC016534; AAH16534.1; -
 DR MGI:1928484; Nudt3.
 DR InterPro: IPR000086; NUDIX_hydrolase.
 DR Pfam: PF00293; NUDIX; 1.
 DR PRINTS; PR00502; NUDIXFAMILY.
 DR PROSITE; PS00893; NUDIX; UNKNOWN_1.
 DR PROSITE; PS00893; NUDIX; UNKNOWN_1.
 KW Hydropathicity. 168 AA; 19029 MW; E543BE5CE520910 CRC64;
 SQ SEQUENCE 168 AA; 51.9%; Score 41; DB 11; Length 168;
 Query Match 53.8%; Pred. No. 28;
 Best Local Similarity 53.8%;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDY 13
 DB 5 KSNQRTYDGDGY 17
 ID Q9X6V5 PRELIMINARY; PRT; 336 AA.
 AC Q9X6V5; PRELIMINARY; PRT; 336 AA.
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE Membrane-bound lytic transglycosylase precursor.
 DE MLTB.
 GN Pseudomonas aeruginosa.
 OS Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OC NCBI_TaxID=287;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=PAO1;
 RC Gagnon L.A.;
 RA Huletsky A.;
 RA "Cloning and characterization of PPB5 of Pseudomonas aeruginosa."
 RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF147448; AAD32232.1; -
 DR HSSP; P41052; 1LTM.
 DR Signal.
 KW SIGNAL
 FT SIGNAL
 FT SIGNAL
 SQ SEQUENCE 336 AA; 37423 MW; IDAFBE8991787BBE CRC64;
 Query Match 51.9%; Score 41; DB 2; Length 336;
 Best Local Similarity 54.5%;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 SVDYDGDSDY 15
 DB 204 AVDFDGDGHIN 214
 ID Q9HX24 PRELIMINARY; PRT; 340 AA.
 AC Q9HX24;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Membrane-bound lytic transglycosylase.

GN MLTB2 OR PA4001.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen";
 RL Nature 406:959-964(2000).
 DR EMBL; AE004817; AAG07388.1; -.
 DR HSP; P41052; LTNW.
 KW Complete proteome.
 SEQUENCE 340 AA; 37867 MW; 7A00BD23A0695BD8 CRC64;
 Query Match 51.9%; Score 41; DB 16; Length 340;
 Best Local Similarity 54.5%; Pred. NO. 63;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 5 SVDYDGDGYM 15
 Db 208 AVDFDGDGHIN 218
 :|||:|
 :|||:|

Search completed: February 14, 2003, 11:18:41
 Job time : 33.3763 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:04:17 ; Search time 18.9677 Seconds
(without alignments)
49.176 Million cell updates/sec

Title: US-09-701-001B-5
Perfect score: 31
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues 908470
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

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18:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
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23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	31	100.0	7	AA70196	Mab 3B9 light chain
2	31	100.0	7	AA70196	Anti-Fas Mab HFE7A
3	31	100.0	7	AA70196	CDR of the light chain
4	31	100.0	7	AA70196	Light chain CDR fo
5	31	100.0	7	AA70196	Mouse anti-Fas ant
6	31	100.0	7	AA70196	Murine anti-Fas an
7	31	100.0	7	AA70196	Antibody 4H5 L cha
8	31	100.0	7	AA70196	Murine CD4/CD34 re
9	31	100.0	7	AA70196	Mouse AC10 antibod
10	31	100.0	7	AA70196	Humanised anti-Fas

11	31	100.0	7	ABB74910	Humanised anti-Fas
12	31	100.0	7	AAU70353	Mouse Kappa III li
13	31	100.0	15	AAU70353	CD-4 antibody varia
14	31	100.0	41	AAU70353	IF7 antibody varia
15	31	100.0	103	AAU70353	Antibody 4H5 L cha
16	31	100.0	103	AAU70353	Murine derived pro
17	31	100.0	106	AAU70353	MaE15 light chain
18	31	100.0	106	AAU70353	Light chain amino
19	31	100.0	111	AAU70353	Immunoglobulin L C
20	31	100.0	111	AAU70353	Mouse anti-HIV mu5
21	31	100.0	111	AAU70353	Mouse-human chim
22	31	100.0	111	AAU70353	Anti HIV antibody
23	31	100.0	111	AAU70353	Chimeric anti HIV
24	31	100.0	111	AAU70353	Light chain variab
25	31	100.0	111	AAU70353	Light chain sequen
26	31	100.0	111	AAU70353	Antibody 4H5 L cha
27	31	100.0	111	AAU70353	Murine derived pro
28	31	100.0	111	AAU70353	Murine derived pro
29	31	100.0	111	AAU70353	Mouse AC10 antibod
30	31	100.0	112	AAU70353	Human x mouse mod
31	31	100.0	112	AAU70353	Monoclonal antibod
32	31	100.0	113	AAU70353	Anti-Leu 3a light
33	31	100.0	115	AAU70353	Amino acids sequen
34	31	100.0	131	AAU70353	Anti-Leu 3a light
35	31	100.0	131	AAU70353	Anti-CD4 antibody
36	31	100.0	131	AAU70353	Humanized antibody
37	31	100.0	131	AAU70353	Humanized antibody
38	31	100.0	131	AAU70353	Variable kappa cha
39	31	100.0	131	AAU70353	Light chain variab
40	31	100.0	131	AAU70353	Light chain variab
41	31	100.0	131	AAU70353	Light chain sequen
42	31	100.0	131	AAU70353	Light chain sequen
43	31	100.0	131	AAU70353	Mouse Mab 3B9 ligh
44	31	100.0	132	AAU70353	Light chain variab
45	31	100.0	132	AAU70353	Light chain sequen

ALIGNMENTS

RESULT 1
AA70196
ID AAR70196 standard; Protein; 7 AA.
XX AAR70196;
AC AC
XX 20-SEP-1995 (first entry)
DT MAB 3B9 light chain CDR.
XX Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy; CDR;
KW complementarity determining region.
XX Mus sp.
OS Mus sp.
XX WO9507301-A.
PN 16-MAR-1995.
PD 07-SEP-1994; 94WO-US10308.
PF 07-SEP-1993; 93US-0117366.
PR 14-OCT-1993; 93US-0136783.
PR (SMIK) SMITHKLINE BEECHAM CORP.
PR (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
XX WPT; 1995-123387/16.
XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived

PT from high affinity mAbs - useful in treatment of IL-4-mediated
 XX and IgE-mediated allergic conditions
 PS Disclosure; Page 55; 97pp; English.

XX Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
 CC chains were cloned into pGEM7f+ and transformed into E. coli
 CC DH5-alpha. A light chain cDNA clone was sequenced (AA083490) that
 CC encoded the protein given in AAR70189. 3 CDRs (AAR70195-97) were
 CC identified.

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 |||||
 1 AASNLES 7

RESULT 2

ID AAW83028 standard; Peptide; 7 AA.

AC AAW83028;

XX 15-MAR-1999 (first entry)

DE Anti-Fas MAB HFE7A light chain CDR-L2.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; complementarity determining region;
 CDR.

XX Mus musculus.

XX AU9859701-A.

XX 08-OCT-1998.

XX 30-MAR-1998; 98AU-0059701.

XX 08-OCT-1997; 97JP-0276064.

XX 01-APR-1997; 97JP-0082953.

XX 25-JUN-1997; 97JP-0169088.

XX (SANY) SANKYO CO LTD.

XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

XX Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX WPI; 1998-543440/47.

XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS

XX Claim 9; Page 185; 292pp; English.

CC This is the amino acid of complementarity determining region 2
 CC (CDR-L2) of the light chain (see AAW83042) of murine anti-human Fas
 CC monoclonal antibody HFE7A. The invention relates to antibodies,
 CC especially humanised antibodies (see AAW83031-37), recognising the
 CC Fas antigen. Such antibodies preferably comprise a heavy chain and
 CC a light chain including CDRs (see AAW83024-29) from the heavy and
 CC light chains of HFE7A. Humanised antibodies are produced by CDR
 CC grafting. The antibodies are capable of inducing apoptosis in
 CC abnormal cells expressing Fas, and of inhibiting Fas-induced
 CC apoptosis in normal cells. They are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's
 CC disease, thrombopenia purpura and insulin-dependent diabetes).
 CC allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and
 CC transplant rejection (all claimed).

SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

|||||

1 AASNLES 7

RESULT 3

AA23773

ID AAY23773 standard; Peptide; 7 AA.

AC AAY23773;

XX 13-SEP-1999 (first entry)

DE CDR of the light chain variable region of antibody 3B9.

XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;
 KW allergy; complementarity determining region.

XX Mus sp.

XX US5928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-0483632.

XX 07-JUN-1995; 95US-0483632.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX 07-SEP-1994; 94WO-US10308.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1999-429500/36.

XX N-PSDB; AAX85890.

XX New DNA molecules encoding recombinant antibodies useful for

PT treating IL4-mediated conditions

XX Example 3; Column 43-44; 50pp; English.

XX The present sequence represents a complementarity determining region (CDR) of the light chain variable region of murine interleukin-4 (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans.

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 20; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 1 AASNLES 7

RESULT 4

AA18115

ID AAY18115 standard; peptide; 7 AA.

AC AAY18115;

XX 11-AUG-1999 (first entry)

DE Light chain CDR for hIL-4 specific antibody.

DE Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease; complementarity determining region; CDR.

OS Synthetic.

XX US5914110-A.

22-JUN-1999.

07-JUN-1995; 95US-0483636.

07-JUN-1995; 95US-0483636.

07-SEP-1993; 93US-0117366.

14-OCT-1993; 93US-0136783.

07-SEP-1994; 94WO-US10308.

(SMIK) SMITHKLINE BEECHAM CORP.

(SMIK) SMITHKLINE BEECHAM PLC.

Gross MS, Holmes SD, Sylvester DR;

WPI; 1999-370482/31.

N-PSDB; AAX79514.

Recombinant IL4 antibodies

Claim 7; Column 43; 50pp; English.

This sequence represents a light chain complementarity determining region (CDR) from an antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis,

CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.

CC The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease.

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 20; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 1 AASNLES 7

RESULT 5

AA14745

ID AAB14745 standard; peptide; 7 AA.

AC AAB14745;

XX 24-NOV-2000 (first entry)

DE Mouse anti-Fas antibody HFE7A light chain CDR2.

DE Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.

OS Mus musculus.

XX JP2000169393-A.

20-JUN-2000.

30-SEP-1999; 99JP-0278301.

30-SEP-1998; 98JP-0276883.

(SANY) SANKYO CO LTD.

WPI; 2000-485645/43.

Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody -

Claim 10; Page 65; 139pp; Japanese.

The invention relates to compositions for the prevention or treatment of diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14744-B14746 represent CDRs 1-3 of the light chain of the murine anti-human Fas monoclonal antibody HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828).

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 21; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 Db 1 AASNLES 7

RESULT 6
 AA90895
 ID AA90895 standard; peptide; 7 AA.
 AC AA90895;
 XX
 DT 08-AUG-2000 (first entry)
 DE Murine anti-Fas antibody peptide fragment #5.
 XX.
 KW Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; anti-rheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Mus musculus.
 XX
 PN EP90663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX
 DR WPI; 2000-258930/23.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX
 PT Disclosure; Page 98; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC anti-rheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in

CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a murine anti-Fas antibody peptide fragment described in the method
 CC of the invention.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 31; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AASNLES 7
 Db 1 AASNLES 7

RESULT 7
 AAY59260
 ID AAY59260 standard; peptide; 7 AA.
 AC AAY59260;
 XX
 DT 17-APR-2000 (first entry)
 DE Antibody 4H5 L chain variable region CDR2 fragment.
 XX
 KW CD4 antigen; anti-human; antibody; 4H5; drug; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN JP11332563-A.
 XX
 PD 07-DEC-1999.
 XX
 PF 26-MAY-1998; 98JP-0163034.
 XX
 PR 26-MAY-1998; 98JP-0163034.
 XX
 PA (ASAH) ASAMI KASEI KOGYO KK.
 XX
 DR WPI; 2000-091351/08.
 XX
 PT An antibody and the nucleic acid coding the antibody -
 XX
 PS Claim 2; Page 14; 25pp; Japanese.
 XX
 CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. Sequences
 CC AAY59259-61 represent the complementarity determining region (CDR)-1,
 CC CDR-2 and CDR-3 fragments in the L chain variable region of the
 CC antibody 4H5 respectively.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 31; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AASNLES 7
 Db 1 AASNLES 7

RESULT 8
 AAY51137
 ID AAY51137 standard; Protein; 7 AA.
 XX
 AC AAY51137;
 XX
 DT 31-MAR-2000 (first entry)

XX DE Murine CD4/CD34 recognizing antibody light chain CDR-2 region #1.
 XX KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 XX KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; complementarity determining region;
 KW CDR-2; light chain; murine.
 XX OS Mus sp.
 XX PN WO9961629-A1.
 XX PD 02-DEC-1999.
 XX PD 24-MAY-1999; 99WO-JP02711.
 XX PF 25-MAY-1998; 98JP-0159957.
 XX PR 26-MAY-1998; 98JP-0163023.
 XX (ASAH) ASAH KASEI KOGYO KK.
 XX (ASAH) ASAH MEDICAL CO LTD.
 XX Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI; 2000-086720/07.
 XX Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells -
 PT Claim 3; Page 77; 111pp; Japanese.
 XX This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived complementarity determining
 CC region CDR-2 protein fragment which is used to illustrate the method of
 CC the invention.
 XX Sequence 7 AA;
 Query Match 100.0%; Score 31; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AASNLES 7
 Db | | | | | | |
 1 AASNLES 7
 RESULT 9
 AAU99854
 ID AAU99854 standard; Peptide; 7 AA.
 XX AC AAU99854;
 XX 07-OCT-2002 (first entry)
 XX Mouse AC10 antibody light chain CDR2 (L2).
 XX Gene therapy; vaccine; CD30 binding; cytostatic; cytotoxic;
 KW Hodgkin's Disease; mouse; AC10 antibody; light chain CDR;
 KW complementarity determining region.
 XX OS Mus musculus.
 XX PN WO200243661-A2.
 XX PD 06-JUN-2002.

XX 28-NOV-2001; 2001WO-US44811.
 XX 28-NOV-2000; 2000US-0724406.
 XX (SEAT-) SEATTLE GENETICS INC.
 XX Francisco JA, Risdon G, Wahl AF, Siegall CB;
 XX WPI; 2002-557522/59.
 XX N-PSDB; ABK88126.
 XX Novel antibody that immunospecifically binds to CD30, useful for
 PT treating Hodgkin's disease, exerts a cytostatic or cytotoxic effect on
 PT Hodgkin's Disease cell line, and is not monoclonal antibody AC10 or
 PT Hefi-1 -
 XX Claim 9; Page 99; 103pp; English.
 XX The invention describes an antibody (I) that immunospecifically binds to
 CC CD30, exerts a cytostatic or cytotoxic effect on Hodgkin's Disease cell
 CC line, and is not monoclonal antibody AC10 or Hefi-1 and does not result
 CC from cleavage of AC10 or Hefi-1 with papain or pepsin. (I), a protein
 CC (II) that competes for CD30 binding with the monoclonal antibodies AC10
 CC or Hefi, or exerts a cytotoxic or cytostatic effect on a Hodgkins'
 CC disease cell line and the nucleic acid encoding the protein (III) are
 CC useful for the treatment or prevention of Hodgkin's Disease in a subject,
 CC by administering (I) to the subject, in the absence of conjugation to a
 CC cytostatic or cytotoxic agent, respectively and a pharmaceutically
 CC acceptable carrier. This is the amino acid sequence of the mouse AC10
 CC antibody light chain complementarity determining region 2 (CDR2), a
 CC polypeptide that competes with AC10 for CD30 binding.
 XX Sequence 7 AA;
 Query Match 100.0%; Score 31; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AASNLES 7
 Db | | | | | | |
 1 AASNLES 7
 RESULT 10
 ABB74864
 ID ABB74864 standard; Peptide; 7 AA.
 XX AC ABB74864;
 XX 26-APR-2002 (first entry)
 XX Humanised anti-Fas antibody related peptide SEQ ID NO 30.
 XX Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
 KW light chain subunit; apoptosis; immunosuppressive; antiallergic;
 KW autoimmune disease; allergy; atopic.
 XX OS Homo sapiens.
 XX JP2001342148-A.
 XX 11-DEC-2001.
 XX 28-MAR-2001; 2001JP-0093106.
 XX 29-MAR-2000; 2000JP-0090918.
 XX (SANY) SANKYO CO LTD.
 XX WPI; 2002-145113/19.
 XX Drug containing humanised anti-Fas antibody, used for preventing and

PT treating autoimmune diseases, allergy, and atopy -
 XX
 PS Example 6 (Preparatory); Page 26; 194pp; Japanese.

XX The invention relates to a preventive or treating agent for diseases
 CC caused by abnormality in Fas/Fas ligand system containing as the active
 CC component an antibody having as the light chain subunit a polypeptide
 CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,
 CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all
 CC fully defined in the specification and having an activity of inducing apoptosis
 CC specifically with mammalian Fas and an activity of inducing apoptosis
 CC in a cell expressing Fas. The agent has immunosuppressive and
 CC antiallergic activity and is used for preventing and treating autoimmune
 CC diseases, allergy, atopy and others. The present sequence is that of a
 CC peptide, useful to the invention.

XX Sequence 7 AA;

SQ Query Match 100.0%; Score 31; DB 23; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 DB 1 AASNLES 7

RESULT 11
 ABB74910
 ID ABB74910 standard; Peptide; 7 AA.

AC ABB74910;

XX 30-APR-2002 (first entry)

XX Humanised anti-Fas antibody related peptide SEQ ID NO 27.

XX Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;
 KW heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;
 KW autoimmune disease; allergy; atopy.

XX Homo sapiens.

XX JP2001342149-A.

XX 11-DEC-2001.

XX 28-MAR-2001; 2001JP-0093243.

XX 29-MAR-2000; 2000JP-0091144.

XX (SANY) SANKYO CO LTD.

XX WPI; 2002-145114/19.

XX Drug for preventing or treating e.g. autoimmune disease or allergy,
 PT comprises humanised anti-Fas antibody -

XX Example 6 (preparatory); Page 26; 154pp; Japanese.

XX The invention relates to a preventive or treating agent for diseases
 CC caused by abnormality in the Fas/Fas ligand system containing, as the
 CC active component, an antibody having a light chain subunit and a heavy
 CC chain subunit and an activity of combining specifically with mammalian
 CC Fas and an activity of inducing apoptosis in a cell expressing Fas. The
 CC agent has antiallergic, immunosuppressive and apoptotic activity and is
 CC used for preventing and treating autoimmune diseases, allergy, atopy and
 CC others. The present sequence is that of a peptide useful to the
 CC invention.

XX Sequence 7 AA;

SQ Query Match 100.0%; Score 31; DB 23; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 DB 1 AASNLES 7

RESULT 12

AAU70353

ID AAU70353 standard; Peptide; 7 AA.

XX AAU70353;

XX 14-FEB-2002 (first entry)

XX Mouse Kappa III light chain CDR2.

XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array;
 KW IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.

XX Mus musculus.

XX WO200183806-A1.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14349.

XX 02-MAY-2000; 2000US-0563222.

XX (EPIC-) EPICYTE PHARM INC.

XX Hiatt AC, Hein MB;

XX WPI; 2002-055482/07.

XX Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array -

XX Disclosure; Page 14; 129pp; English.

XX The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that
 CC binds to a ligand, and transformed plant cells are selected, and
 CC preparing an IgBP array in plant cells. At least one peptide sequence has
 CC at least 75% sequence identity to a framework region (FR) of a native
 CC IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule.
 CC The method is useful for preparing an immunoglobulin binding protein
 CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic
 CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)
 CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The
 CC CHBP is useful for discovery of e.g. screening assays of IgBPs having
 CC desired characteristics. The present sequence is a mammalian
 CC immunoglobulin derived peptide that may be incorporated into an IgBP of
 CC the invention.

XX Sequence 7 AA;

SQ Query Match 100.0%; Score 31; DB 23; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 DB 1 AASNLES 7

RESULT 13
AAR66144
ID AAR66144 standard; peptide; 15 AA.

XX AC AAR66144;
XX 12-JUL-1995 (first entry)
XX CD-4 antibody variable region complementary peptide.
XX CD-4 antibody variable region; complementary peptide;
KW extra-corporeal blood circulation; cell filter material.
XX Synthetic.

XX JP06269663-A.

XX 27-SEP-1994.

XX 17-MAR-1993; 93JP-0057206.

XX 17-MAR-1993; 93JP-0057206.

XX (TOYM) TOYOBO KK.

XX WPI; 1994-346316/43.

XX Material for collecting cells positive for CD-4 antibody -
PT comprises nonwoven fabric having keto-alkyl halide functional gp
XX Example 2; Page 7; 9pp; Japanese.

XX AAR66140-R66146 are peptides complementary to the variable region
CC of the CD-4 antibody, these peptides are fixed onto a claimed
CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with
CC keto-alkyl halide functional groups. This material can be used
CC as a filter for CD-4 positive cells in a medical treatment
CC involving the extra-corporeal circulation of blood.

XX Sequence 15 AA;

Query Match 100.0%; Score 31; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AASNLES 7
| | | | |
9 AASNLES 15

DB

RESULT 14
AAY91015
ID AAY91015 standard; protein; 41 AA.

XX AC AAY91015;

XX 05-SEP-2000 (first entry)

XX 1F7 antibody variable light chain L2 amino acid sequence SEQ ID NO:6.
DE
XX 1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection;
KW AIDS; anti-HIV; human immunodeficiency virus; detection;
KW acquired immunodeficiency syndrome.

XX Mus sp.

XX US6057421-A.

XX 02-MAY-2000.

XX 03-DEC-1997; 97US-0984277.

XX 30-NOV-1994; 94US-0351193.

XX (IMMP-) IMMIPHERON INC.

XX Muller S, Kohler H;

XX WPI; 2000-338622/29.

XX Variable heavy and light chain regions of murine monoclonal antibody
PT 1F7, useful for treating HIV infection and AIDS -

XX Claim 1; Fig 8; 45pp; English.

XX The present invention describes the variable heavy and light chain
CC regions (I) of murine monoclonal antibody (mAb) 1F7. AAY91014 to
CC AAY91016 represent specifically claimed amino acid sequences of the
CC variable light chain, and AAY91017 to AAY91019 represent specifically
CC claimed amino acid sequence of the variable heavy chain. The antibodies
CC are used for treatment of HIV (human immunodeficiency virus) infection
CC and AIDS (acquired immunodeficiency syndrome). They are also used for
CC detecting HIV in serum and for stimulating HIV antigen related and
CC committed B cells to produce broadly reactive and neutralising antibodies
CC by clonotypic stimulation.

XX Sequence 41 AA;

Query Match 100.0%; Score 31; DB 21; Length 41;
Best Local Similarity 100.0%; Pred. No. 6.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
| | | | |

DB 12 AASNLES 18

RESULT 15
AAY59263
ID AAY59263 standard; protein; 103 AA.

XX AC AAY59263;

XX 17-APR-2000 (first entry)

XX Antibody 4H5 L chain variable region.

XX CD4 antigen; anti-human; antibody; 4H5; drug.

XX Mus sp.

XX JP11332563-A.

XX 07-DEC-1999.

XX 26-MAY-1998; 98JP-0163034.

XX 26-MAY-1998; 98JP-0163034.

XX (ASAH) ASAH KASEI KOGYO KK.

XX WPI; 2000-091351/08.

XX N-PSDB; AAZ59662.

XX An antibody and the nucleic acid coding the antibody -

XX Claim 5; Page 15-16; 25pp; Japanese.

XX The invention provides an antibody having affinity to CD4 antigen. The
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
CC application for drugs. It is highly safe in human dose. The present
CC sequence represents the L chain variable region of the antibody 4H5.

XX Sequence 103 AA;

Query Match 100.0%; Score 31; DB 21; Length 103;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7
| | | | |
Db 46 AASNLES 52

Search completed: February 14, 2003, 11:15:45
Job time : 19.9677 secs

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Title: US-09-701-001B-5
Perfect score: 31
Sequence: 1 AASNLES 7
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Local number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	31	100.0	7	US-08-483-636-18	Sequence 18, Appl
2	31	100.0	7	US-08-483-632-18	Sequence 18, Appl
3	31	100.0	41	US-08-984-277-6	Sequence 6, Appl
4	31	100.0	106	US-08-466-151-6	Sequence 6, Appl
5	31	100.0	106	US-08-466-163B-6	Sequence 6, Appl
6	31	100.0	111	US-08-491-845-8	Sequence 8, Appl
7	31	100.0	111	US-08-491-845-16	Sequence 16, Appl
8	31	100.0	111	US-08-483-636-73	Sequence 73, Appl
9	31	100.0	111	US-08-483-632-73	Sequence 73, Appl
10	31	100.0	115	US-08-513-968-51	Sequence 51, Appl
11	31	100.0	131	US-08-483-636-14	Sequence 14, Appl
12	31	100.0	131	US-08-483-636-58	Sequence 58, Appl
13	31	100.0	131	US-08-483-632-14	Sequence 14, Appl
14	31	100.0	131	US-08-483-632-58	Sequence 58, Appl
15	31	100.0	131	US-08-589-939-3	Sequence 3, Appl
16	31	100.0	131	US-08-579-378A-14	Sequence 14, Appl
17	31	100.0	131	US-08-579-378A-18	Sequence 18, Appl
18	31	100.0	132	US-08-483-636-2	Sequence 2, Appl
19	31	100.0	132	US-08-483-632-2	Sequence 2, Appl
20	31	100.0	218	PCT-US96-13152-2	Sequence 11, Appl
21	28	90.3	7	US-08-650-262-11	Sequence 11, Appl
22	28	90.3	98	US-08-881-037-75	Sequence 75, Appl
23	28	90.3	108	US-08-650-262-2	Sequence 2, Appl
24	28	90.3	120	US-08-111-080-24	Sequence 24, Appl
25	28	90.3	120	US-08-211-980-24	Sequence 24, Appl
26	28	90.3	120	PCT-US93-07967-24	Sequence 24, Appl
27	27	87.1	6	US-08-137-117D-137	Sequence 137, App

28	27	87.1	6	US-08-436-717-137	Sequence 137, App
29	27	87.1	7	US-09-425-638A-70	Sequence 70, Appl
30	27	87.1	7	US-09-543-004-70	Sequence 70, Appl
31	27	87.1	17	US-08-712-212-5	Sequence 5, Appli
32	27	87.1	17	PCT-US95-05160-5	Sequence 5, Appli
33	27	87.1	20	US-09-556-605-19	Sequence 19, Appl
34	27	87.1	20	US-09-556-605-20	Sequence 20, Appl
35	27	87.1	64	US-08-765-179B-10	Sequence 10, Appl
36	27	87.1	106	US-08-202-047-26	Sequence 26, Appl
37	27	87.1	106	US-08-964-690-26	Sequence 26, Appl
38	27	87.1	109	US-09-157-370-3	Sequence 3, Appli
39	27	87.1	109	US-09-425-638A-20	Sequence 20, Appl
40	27	87.1	109	US-09-425-638A-21	Sequence 21, Appl
41	27	87.1	109	US-09-425-638A-39	Sequence 39, Appl
42	27	87.1	109	US-09-425-638A-40	Sequence 40, Appl
43	27	87.1	109	US-09-425-638A-41	Sequence 41, Appl
44	27	87.1	109	US-09-425-638A-42	Sequence 42, Appl
45	27	87.1	109	US-09-425-638A-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-483-636-18
; Sequence 18, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-483-636-18

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7
| | | | |
Db 1 AASNLES 7

RESULT 2

US-08-483-632-18
; Sequence 18, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-483-632-18

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7
| | | | |
Db 1 AASNLES 7

RESULT 3

US-08-984-277-6

; Sequence 6, Application US/08984277
; Patent No. 6057421
; GENERAL INFORMATION:
; APPLICANT: Muller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: VARIABLE HEAVY AND LIGHT CHAIN REGIONS OF MURINE
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1F7
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,277
; FILING DATE: 3-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca, Daniel
; REGISTRATION NUMBER: 42,368
; REFERENCE/DOCKET NUMBER: 50200-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-756-8600
; TELEFAX: 202-756-8699
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

US-08-984-277-6

Query Match 100.0%; Score 31; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7
| | | | |
Db 12 AASNLES 18

RESULT 4

US-08-466-151-6
; Sequence 6, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

US-08-466-151-6

us-09-701-001b-5-rai

Fri Feb 14 15:00:56 2003

SOFTWARE: WinPattn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/466,151
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/466163
 FILING DATE: 06-Jun-1995
 APPLICATION NUMBER: 08/405617
 FILING DATE: 15-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/185899
 FILING DATE: 26-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/879495
 FILING DATE: 07-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/744768
 FILING DATE: 14-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Svoboda, Craig G.
 REGISTRATION NUMBER: 39,044
 REFERENCE/DOCKET NUMBER: P0718P2C1D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1489
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 106 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-466-151-6

Query Match 100.0%; Score 31; DB 3; Length 106;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7
 Db 54 AASNLES 60

RESULT 5
 US-08-466-163B-6
 ; Sequence 6, Application US/08466163B
 ; Patent No. 6329509
 ; GENERAL INFORMATION:
 ; APPLICANT: Jardieu, Paula M.
 ; TITLE OF INVENTION: Immunoglobulin Variants
 ; FILE REFERENCE: P0718P2C1D1
 ; CURRENT APPLICATION NUMBER: US/08/466,163B
 ; CURRENT FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: US 08/405,617
 ; PRIOR FILING DATE: 1995-03-15
 ; PRIOR APPLICATION NUMBER: US 08/185,899
 ; PRIOR FILING DATE: 1994-01-26
 ; PRIOR APPLICATION NUMBER: US 07/879,495
 ; PRIOR FILING DATE: 1992-05-07
 ; PRIOR APPLICATION NUMBER: US 07/744,768
 ; PRIOR FILING DATE: 1991-08-14
 ; NUMBER OF SEQ ID NOS: 64
 ; SEQ ID NO 6
 ; LENGTH: 106
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-08-466-163B-6

Query Match 100.0%; Score 31; DB 4; Length 106;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7

Db 54 AASNLES 60

RESULT 6
 US-08-491-845-8
 ; Sequence 8, Application US/08491845
 ; Patent No. 5773247
 ; GENERAL INFORMATION:
 ; APPLICANT: MAEDA, Hiroaki
 ; APPLICANT: KIMACHI, Kazuhiko
 ; APPLICANT: EDA, Yasuyuki
 ; APPLICANT: SHIOSAKI, Kouichi
 ; APPLICANT: OSATOMI, Kiyoshi
 ; APPLICANT: TOKIYOSHI, Sachio
 ; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
 ; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Browdy and Neimark
 ; STREET: 419 Seventh Street N.W. Ste. 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/491,845
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/JP93/00039
 ; FILING DATE: 14-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Browdy, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: MAEDA=5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 628-5197
 ; TELEFAX: (202) 737-3528
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 111 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-491-845-8

Query Match 100.0%; Score 31; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7
 Db 54 AASNLES 60

RESULT 7
 US-08-491-845-16
 ; Sequence 16, Application US/08491845
 ; Patent No. 5773247
 ; GENERAL INFORMATION:
 ; APPLICANT: MAEDA, Hiroaki
 ; APPLICANT: KIMACHI, Kazuhiko
 ; APPLICANT: EDA, Yasuyuki
 ; APPLICANT: SHIOSAKI, Kouichi
 ; APPLICANT: OSATOMI, Kiyoshi
 ; APPLICANT: TOKIYOSHI, Sachio
 ; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND

;; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Browdy and Neimark
;; STREET: 419 Seventh Street N.W. Ste. 300
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/491,845
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/JP93/00039
;; FILING DATE: 14-JAN-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Browdy, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: MAEDA-5
;; TELEPHONE: (202) 628-5197
;; TELEFAX: (202) 737-3528
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 111 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-491-845-16

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 54 AASNLES 60

RESULT 8
US-08-483-636-73
; Sequence 73, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/117366
;; FILING DATE: 07-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/136783
;; FILING DATE: 14-OCT-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US/94/10308
;; FILING DATE: 07-SEP-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sutton, Jeffrey A.
;; REGISTRATION NUMBER: 34,028
;; REFERENCE/DOCKET NUMBER: P50186-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 270-5024
;; TELEFAX: (215) 270-5090
;; INFORMATION FOR SEQ ID NO: 73:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 111 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-483-636-73

Query Match 100.0%; Score 31; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 54 AASNLES 60

RESULT 9
US-08-483-632-73
; Sequence 73, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-483-632-73

Query Match 100.0%; Score 31; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AASNLES 7
|||||||
54 AASNLES 60

RESULT 10
US-08-513-968-51
; Sequence 51, Application US/08513968
; Patent No. 6114143
; GENERAL INFORMATION:
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: MAKIZUMI, Keiichi
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: TORIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NETMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,968
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 78913/1993
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EDA-1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-513-968-51

Query Match 100.0%; Score 31; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||||
Db 58 AASNLES 64

RESULT 11
US-08-483-636-14
; Sequence 14, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-636-14

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||||
Db 73 AASNLES 79

RESULT 12
US-08-483-636-58
; Sequence 58, Application US/08483636

; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-636-58

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7
Db 73 AASNLES 79

RESULT 13
US-08-483-632-14
; Sequence 14, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:

; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-632-14

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7
Db 73 AASNLES 79

RESULT 14
US-08-483-632-58
; Sequence 58, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-632-58

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.4; 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 73 AASNLES 79

RESULT 15
US-08-589-939-3
Sequence 3, Application us/08589939
Patent No. 6015662
GENERAL INFORMATION:
APPLICANT: Hackett, Jr., John R.
APPLICANT: Hoff, Jane A.
APPLICANT: Ostrow, David H.
APPLICANT: Golden, Alan M.
TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND
TITLE OF INVENTION: CONTROLS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: US
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: .US/08/589,939
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5865.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-935-1729
TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-589-939-3

Query Match 100.0%; Score 31; DB 3; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 74 AASNLES 80

Search completed: February 14, 2003, 11:20:50
Job time : 7.32258 secs

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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:15:53 ; Search time 4.06452 Seconds
(without alignments)
44.001 Million cell updates/sec

Title: US-09-701-001B-5
Perfect score: 31
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata1/pubpaa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata1/pubpaa/US07_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata1/pubpaa/US09_NEW_PUB.pep.*
- 9: /cgn2_6/ptodata1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata1/pubpaa/US10_NEW_PUB.pep.*
- 11: /cgn2_6/ptodata1/pubpaa/US10_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	31	100.0	7	9	US-09-879-461-18
2	31	100.0	106	10	US-09-802-077-6
3	31	100.0	106	10	US-09-802-096-6
4	31	100.0	131	9	US-09-879-461-14
5	31	100.0	131	9	US-09-879-461-58
6	31	100.0	132	9	US-09-879-461-2
7	31	100.0	218	10	US-09-917-410-2
8	31	100.0	238	9	US-09-903-327A-4
9	28	90.3	111	9	US-09-144-886-93
10	28	90.3	112	9	US-09-144-886-95
11	27	87.1	20	10	US-09-839-447A-19
12	27	87.1	20	10	US-09-839-447A-20
13	27	87.1	112	9	US-09-144-886-80
14	27	87.1	112	9	US-09-144-886-81
15	27	87.1	112	9	US-09-144-886-84
16	27	87.1	112	9	US-09-144-886-85
17	27	87.1	112	9	US-09-144-886-86
18	27	87.1	112	9	US-09-144-886-94
19	27	87.1	112	10	US-09-810-502-36

20	87.1	112	10	US-09-810-502-37	Sequence 37, Appl
21	87.1	129	10	US-09-839-447A-2	Sequence 2, Appli
22	87.1	619	10	US-09-800-065-2	Sequence 2, Appli
23	83.9	108	10	US-09-056-160B-12	Sequence 12, Appl
24	83.9	109	10	US-09-811-123-6	Sequence 6, Appli
25	83.9	111	10	US-09-920-171-7	Sequence 7, Appli
26	83.9	263	9	US-09-956-086-3	Sequence 3, Appli
27	83.9	263	9	US-09-956-087-3	Sequence 3, Appli
28	83.9	283	9	US-09-985-442-6	Sequence 6, Appli
29	83.9	283	10	US-09-983-580-6	Sequence 6, Appli
30	83.9	721	10	US-09-727-801-14	Sequence 14, Appl
31	80.6	105	10	US-09-864-761-38594	Sequence 38594, A
32	80.6	518	10	US-09-841-132-333	Sequence 333, App
33	80.6	554	10	US-09-864-761-37625	Sequence 37625, A
34	80.6	875	10	US-09-848-035-16	Sequence 16, Appl
35	80.6	875	10	US-09-986-224-16	Sequence 16, Appl
36	80.6	894	9	US-09-754-853A-1099	Sequence 1099, Ap
37	80.6	894	9	US-09-754-853A-1116	Sequence 1116, Ap
38	80.6	894	9	US-09-754-853A-1117	Sequence 1117, Ap
39	80.6	894	9	US-09-754-853A-1118	Sequence 1118, Ap
40	80.6	894	9	US-09-754-853A-1119	Sequence 1119, Ap
41	80.6	1751	10	US-09-841-132-445	Sequence 445, App
42	80.6	1751	10	US-09-841-132-594	Sequence 594, App
43	80.6	1752	10	US-09-841-132-180	Sequence 180, App
44	80.6	3256	10	US-09-919-172-98	Sequence 98, Appl
45	77.4	7	9	US-09-968-561A-185	Sequence 185, App

ALIGNMENTS

RESULT 1

US-09-879-461-18

; Sequence 18, Application US/09879461

; Publication No. US20020193575A1

; GENERAL INFORMATION:

; APPLICANT: Holmes, Stephen D.

; Gross, Mitchell S.

; Sylvester, Daniel R.

; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in Treatment of IL4 Mediated Disorders

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: Corporate Intellectual Property, UW2220 - 709

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406-2799

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/879,461

; FILING DATE: 12-Jun-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/612,929

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/136,783

; FILING DATE: 14-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Sutton, Jeffrey A.

; REGISTRATION NUMBER: 34,028

; REFERENCE/DOCKET NUMBER: P50186-2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 270-5024

; TELEFAX: (215) 270-5090

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-879-461-18

Query Match 100.0%; Score 31; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
| | | | |
Db 1 AASNLES 7

RESULT 2

US-09-802-077-6
; Sequence 6, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C20S
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 6
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-6

Query Match 100.0%; Score 31; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
| | | | |
54 AASNLES 60

RESULT 3

US-09-802-096-6
; Sequence 6, Application US/09802096
; Patent No. US20010033839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C30S
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768

; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 6
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-6

Query Match 100.0%; Score 31; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
| | | | |
Db 54 AASNLES 60

RESULT 4

US-09-879-461-14
; Sequence 14, Application US/09879461
; Publication No. US20020193575A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; Gross, Mitchell S.
; Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property, UW2220 - 709
; Swedeland Rd.
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-879-461-14

Query Match 100.0%; Score 31; DB 9; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
| | | | |
Db 73 AASNLES 79

RESULT 5
US-09-879-461-58
; Sequence 58, Application US/09879461
; Publication No. US20020193575A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; Gross, Mitchell S.
; Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property, UW2220 - 709
; Swedeland Rd.
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-879-461-58
Query Match 100.0%; Score 31; DB 9; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AASNLES 7
Db 73 AASNLES 79
RESULT 6
US-09-879-461-2
; Sequence 2, Application US/09879461
; Publication No. US20020193575A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; Gross, Mitchell S.
; Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation

STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-879-461-2
Query Match 100.0%; Score 31; DB 9; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AASNLES 7
Db 74 AASNLES 80
RESULT 7
US-09-917-410-2
; Sequence 2, Application US/09917410
; Patent No. US20020098183A1
; GENERAL INFORMATION:
; APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
; CO, Man S.
; TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
; MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
; PREVENTION OF ACUTE ORGAN DAMAGE AFTER
; EXTRACORPOREAL BLOOD CIRCULATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII, WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/917,410
; FILING DATE: 26-Jul-2001
; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/578,953
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: EP 95 114 969.9
;; FILING DATE: 19-Sep-95
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. US20020098183Alman D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-8200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 218
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-917-410-2

Query Match 100.0%; Score 31; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 54 AASNLES 60

RESULT 8
US-09-903-327A-4
; Sequence 4, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erquang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
US-09-903-327A-4

Query Match 100.0%; Score 31; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 74 AASNLES 80

RESULT 9
US-09-144-886-93
; Sequence 93, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D

;; APPLICANT: Amersdorfer, Peter
;; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
;; FILE REFERENCE: 2500.117USO
;; CURRENT APPLICATION NUMBER: US/09/144,886
;; CURRENT FILING DATE: 1998-08-31
;; NUMBER OF SEQ ID NOS: 98
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 93
;; LENGTH: 111
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
;; OTHER INFORMATION: ICG region VL epitope 3
US-09-144-886-93

Query Match 90.3%; Score 28; DB 9; Length 111;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 54 AASNLES 60

RESULT 10
US-09-144-886-95
; Sequence 95, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: ICG region VL epitope 3
US-09-144-886-95

Query Match 90.3%; Score 28; DB 9; Length 112;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 54 AASNLES 60

RESULT 11
US-09-839-447A-19
; Sequence 19, Application US/09839447A
; Patent No. US20020058247A1
; GENERAL INFORMATION:
; APPLICANT: Sallberg, Matti
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
; FILE REFERENCE: TRIPEP.020CPI
; CURRENT APPLICATION NUMBER: US/09/839,447A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/556605
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 19
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-09-839-447A-19

Query Match      87.1%; Score 27; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 ASNLES 7
Db  15 ASNLES 20

RESULT 12
US-09-839-447A-20
; Sequence 20, Application US/09839447A
; Patent No. US20020058247A1
; GENERAL INFORMATION:
; APPLICANT: Saliberg, Matti
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
; TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
; FILE REFERENCE: TRIPEP.020CP1
; CURRENT APPLICATION NUMBER: US/09/839,447A
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/556605
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-09-839-447A-20

Query Match      87.1%; Score 27; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 ASNLES 7
   5 ASNLES 10

RESULT 13
US-09-144-886-80
; Sequence 80, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 1B6 region VL epitope 1
US-09-144-886-80

Query Match      87.1%; Score 27; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 ASNLES 7
   5 ASNLES 60

RESULT 14
US-09-144-886-81
; Sequence 81, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 1C9 region VL epitope 1
US-09-144-886-81

Query Match      87.1%; Score 27; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 ASNLES 7
   5 ASNLES 60

RESULT 15
US-09-144-886-84
; Sequence 84, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 1A1 region VL epitope 2
US-09-144-886-84

Query Match      87.1%; Score 27; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 ASNLES 7
   5 ASNLES 60

Search completed: February 14, 2003, 11:21:31
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Fri Feb 14 15:00:57 2003

us-09-701-001b-5.rapb

Page 6

Job time : 4.06452 secs

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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:12:02 ; Search time 7 seconds
(without alignments)

96.134 Million cell updates/sec

Title: US-09-701-001b-5

Perfect score: 31

Sequence: 1 AASNLES 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pirl:*

2: pirl2:*

3: pirl3:*

4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	65	2 C38601	Ig kappa chain V r
2	31	100.0	65	2 B38601	Ig kappa chain V r
3	31	100.0	93	2 A38601	Ig kappa chain V r
4	31	100.0	110	1 KVM510	Ig kappa chain V r
5	31	100.0	111	1 KVM5C1	Ig kappa chain V r
6	31	100.0	111	1 KVM543	Ig kappa chain V r
7	31	100.0	111	1 KVM583	Ig kappa chain V r
8	31	100.0	111	1 KVM589	Ig kappa chain V r
9	31	100.0	112	2 S19971	Ig kappa chain V r
10	31	100.0	112	2 S19976	Ig kappa chain V r
11	31	100.0	131	2 PH1226	Ig kappa chain pre
12	31	100.0	463	2 B64160	hypothetical prote
13	31	100.0	942	2 T39624	6-phosphofructokin
14	31	100.0	1208	2 T00362	hypothetical prote
15	28	90.3	69	2 AH3440	cold shock protein
16	28	90.3	108	1 KIHUGL	Ig kappa chain V-I
17	28	90.3	112	2 S19972	Ig kappa chain V r
18	28	90.3	122	2 S06731	Ig kappa chain pre
19	28	90.3	122	2 S40370	Ig kappa chain - h
20	28	90.3	209	2 C87521	hypothetical prote
21	28	90.3	228	2 A98166	hypothetical prote
22	28	90.3	228	2 AF3121	hypothetical prote
23	28	90.3	313	1 QMXRWT	capsomere protein
24	28	90.3	313	1 QMXRWN	nonstructural prot
25	28	90.3	579	2 AB2177	hypothetical prote
26	28	90.3	632	2 D71941	ATP-dependent zinc
27	28	90.3	784	1 A55236	kinesin-related pr
28	27	87.1	81	2 S42193	Ig kappa chain V r
29	27	87.1	91	2 S25462	- Ig kappa chain V r

ALIGNMENTS

RESULT 1

C38601

Ig kappa chain V region (2B5) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999

C:Accession: C38601

R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A:Title: Common structural features among monoclonal antibodies binding the same anti

A:Reference number: A38601; MUID:91115823; PMID:1703527

A:Accession: C38601

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-65 <GOS>

A:Cross-references: GB:M57980; NID:g196406; PIDN:AAA63361.1; PID:g196407

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 65;

Best Local Similarity 100.0%; Pred. No. 0.87; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

Db 7 AASNLES 13

RESULT 2

B38601

Ig kappa chain V region (7D4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999

C:Accession: B38601

R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A:Title: Common structural features among monoclonal antibodies binding the same anti

A:Reference number: A38601; MUID:91115823; PMID:1703527

A:Accession: B38601

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-65 <GOS>

A:Cross-references: GB:M57979; NID:g196404; PIDN:AAA63360.1; PID:g196405

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 65;

Best Local Similarity 100.0%; Pred. No. 0.87; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

Db 7 AASNLES 13

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
| | | | | | |
Db 54 AASNLES 60

RESULT 6

QVMS43
Ig kappa chain V region (PC7043) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C:Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Accession: A01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42187
A:Molecule type: DNA
A:Residues: 10-99 <MOJ>
A:Cross-references: EMBL:Z25444; NID:g407832; PIDN:CAA80931.1; PID:g407833
A:Note: V-kappa-2IE; anti-collagen
A:Accession: S42194
A:Molecule type: DNA
A:Residues: 12-99 <MOJ>
A:Cross-references: EMBL:Z25458; NID:g407844; PIDN:CAA80945.1; PID:g407845
A:Note: V-kappa-2IE; anti-collagen
A:Accession: S42190
A:Molecule type: DNA
A:Residues: 13-99 <MOJ>
A:Cross-references: EMBL:Z25450; NID:g407838; PIDN:CAA80937.1; PID:g407839
A:Note: V-kappa-2IE; anti-collagen
A:Accession: S42189
A:Molecule type: DNA
A:Residues: 15-99 <MOA>
A:Cross-references: EMBL:Z25448; NID:g407836; PIDN:CAA80935.1; PID:g407837
A:Note: V-kappa-2IE; anti-collagen
A:Accession: S42188
A:Molecule type: DNA
A:Residues: 12-99 <MOJ>
A:Cross-references: EMBL:Z25446; NID:g407834; PIDN:CAA80933.1; PID:g407835
A:Note: V-kappa-2IE; anti-collagen
A:Accession: S42191
A:Molecule type: DNA
A:Residues: 10-99 <MOY>
A:Cross-references: EMBL:Z25452; NID:g407840; PIDN:CAA80939.1; PID:g407841
A:Note: V-kappa-2IE; anti-collagen
A:Accession: S42192
A:Molecule type: DNA
A:Residues: 10-99 <MOJ>
A:Cross-references: EMBL:Z25454; NID:g407842; PIDN:CAA80941.1; PID:g407843
A:Note: V-kappa-2IE; anti-collagen
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

RESULT 3

A38601
Ig kappa chain V region (IG3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: A38601

R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: A38601
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-93 <GOS>
A:Cross-references: GB:M57978; NID:g196402; PIDN:AAA63359.1; PID:g196403
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
| | | | | | |
Db 35 AASNLES 41

RESULT 4

QVMS10
Ig kappa chain V region (PC7210) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: D01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Accession: D01937
A:Molecule type: protein
A:Residues: 1-110 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
| | | | | | |
Db 54 AASNLES 60

RESULT 5

QVMSC1
Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000
C:Accession: A01936
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978

A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related mo
A:Reference number: A93822; MUID:79012520; PMID:99744
A:Accession: A01936
A:Molecule type: protein
A:Residues: 1-111 <MCK>
A:Comment: This chain was isolated from a myeloma protein.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||||
Db 54 AASNLES 60

RESULT 7

KVMS83
Ig kappa chain V region (PC7183) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: B01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Gene 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: B01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||||
Db 54 AASNLES 60

RESULT 8

KVMS69
Ig kappa chain V region (PC7769) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: A01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Gene 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: B01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||||
Db 54 AASNLES 60

RESULT 9

S19971
Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

C:Accession: S19971; S19973
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
Submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19971
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65091; NID:g52288; PIDN:CAA46219.1; PID:g52289
A:Experimental source: clone M-T310
A:Accession: S19973
A:Molecule type: mRNA
A:Residues: 1-112 <WEW>
A:Cross-references: EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PID:g52293
A:Experimental source: M-T404
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||||
Db 54 AASNLES 60

RESULT 10

S19976
Ig kappa chain V region (M-T413) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19976
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
Submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19976
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID:g52299
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||||
Db 54 AASNLES 60

RESULT 11

PH1226
Ig kappa chain precursor V region (M-T310) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C:Accession: PH1226
R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; L. Gene 121, 271-278, 1992
A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and CD8 epitopes.
A:Reference number: PH1224; MUID:93077041; PMID:1446824

A:Accession: PH1226
A:Molecule type: mRNA
A:Residues: 1-131 <WEI>

A:Cross-references: GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:g260766
A:Note: this mouse sequence was hybridized and fused with a human constant region gene.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-131/Product: Ig light chain V region #status predicted <MAT>
F;36-114/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||
Db 74 AASNLES 80

RESULT 12

B64160
hypothetical protein HI0852 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
C:Accession: B64160
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
M.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: B64160
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-463 <TIGR>
A:Cross-references: GB:U32766; GB:L42023; NID:gl573854; PIDN:AAC22509.1; PID:gl573866; T
A:Note: best homolog was a hypothetical protein from Escherichia coli
C:Superfamily: multidrug-efflux transporter
C:Keywords: antibiotic resistance; transmembrane protein

Query Match 100.0%; Score 31; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||
Db 94 AASNLES 100

RESULT 13

T39624
6-phosphofructokinase beta subunit - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C:Accession: T39624
R;Good, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
Submitted to the EMBL Data Library, March 1998
A:Reference number: 221843
A:Accession: T39624
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-942 <WOO>
A:Cross-references: EMBL:AL022104; PIDN:CAA17900.1; GSPDB:GN00067; SPDB:SPBC16H5.02
A:Experimental source: strain 972h; cosmid c16H5
C:Genetics:
A:Gene: SPDB:SPBC16H5.02
A:Map position: 2
C:Superfamily: human 6-phosphofructokinase; 6-phosphofructokinase 1 homology

Query Match 100.0%; Score 31; DB 2; Length 942;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||
Db 165 AASNLES 171

RESULT 14

T00362
hypothetical protein KIAA0675 - human
C:Species: Homo sapiens (man)
C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 02-Sep-2000
C:Accession: T00362
R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura,
DNA Res. 5, 169-176, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. X. The compl
A:Reference number: Z14142; MUID:98403880; PMID:9734811
A:Accession: T00362
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1208 <ISH>
A:Cross-references: EMBL:AB014575; NID:g3327163; PIDN:BAA31650.1; PID:g3327164
A:Experimental source: brain; clone HK02566
C:Genetics:
A:Note: KIAA0675
C:Superfamily: RING finger homology
F;1144-1193/Domain: RING finger homology <RRN>

Query Match 100.0%; Score 31; DB 2; Length 1208;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||
Db 896 AASNLES 902

RESULT 15

AH3440
cold shock protein csps [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 17-May-2002
C:Accession: AH3440
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagi, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AD3252; PMID:11756688
A:Accession: AH3440
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-69 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL52691.1; PID:gl7983518; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1510
A:Map position: 1
C:Superfamily: major cold shock protein; cold shock domain homology

Query Match 90.3%; Score 28; DB 2; Length 69;
Best Local Similarity 85.7%; Pred. No. 5.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
|||||
Db 62 AASNLES 68

Search completed: February 14, 2003, 11:19:47
Job time : 7 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model
Run on: February 14, 2003, 11:05:27 ; Search time 3.6129 Seconds
(without alignments)
80.360 Million cell updates/sec

Title: US-09-701-001b-5
Perfect score: 31
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match %	Length	DB ID	Description
1	31	100.0	110	1 KV3P_MOUSE	P01668 mus musculus
2	31	100.0	111	1 KV3L_MOUSE	P01664 mus musculus
3	31	100.0	111	1 KV3M_MOUSE	P01665 mus musculus
4	31	100.0	111	1 KV3N_MOUSE	P01666 mus musculus
5	31	100.0	111	1 KV3Q_MOUSE	P01669 mus musculus
6	31	100.0	463	1 YIEO_HAEIN	P44903 haemophilus
7	28	90.3	108	1 KV1G_HUMAN	P01599 homo sapien
8	28	90.3	313	1 VP9_WTV	P12326 wound tumor
9	28	90.3	313	1 FTSH_HELPJ	P31611 wound tumor
10	28	90.3	632	1 KL68_DROME	Q92m66 helicobacte
11	28	90.3	784	1 KV1B_HUMAN	P01594 homo sapien
12	27	87.1	108	1 KV3V_MOUSE	P01674 mus musculus
13	27	87.1	108	1 KV3H_MOUSE	P01660 mus musculus
14	27	87.1	111	1 KV3J_MOUSE	P01662 mus musculus
15	27	87.1	111	1 KV3K_MOUSE	P01663 mus musculus
16	27	87.1	111	1 KV3L_MOUSE	P01667 mus musculus
17	27	87.1	111	1 KV3O_MOUSE	P01670 mus musculus
18	27	87.1	111	1 KV3S_MOUSE	P01671 mus musculus
19	27	87.1	111	1 KV3T_MOUSE	P01672 mus musculus
20	27	87.1	131	1 KV3I_MOUSE	P01661 mus musculus
21	27	87.1	177	1 PSS_BACSU	P39823 bacillus su
22	27	87.1	230	1 CUT1_FUSSO	P00590 fusarium so
23	27	87.1	230	1 CUT1_FUSSC	Q99174 fusarium so
24	27	87.1	336	1 UPPS_BACSU	O31751 bacillus su
25	27	87.1	396	1 PGK_LISIN	Q92810 listeria in
26	27	87.1	396	1 PGK_LISMO	Q8y4i2 listeria mo
27	27	87.1	486	1 YN8U_YEAST	P53742 saccharomyc
28	27	87.1	661	1 UVRB_RICCN	Q92j03 rickettsia
29	27	87.1	662	1 UVRB_RICPR	Q92dw2 rickettsia
30	27	87.1	689	1 UVRB_HALN1	Q9hmt9 halobacteri
31	26	83.9	112	1 KV3G_MOUSE	P01659 mus musculus
32	26	83.9	132	1 KV3F_MOUSE	P01658 mus musculus
33	26	83.9	132	1 KV3E_MOUSE	P01658 mus musculus

34	26	83.9	292	1 SNAP_DROME	Q23983 drosophila
35	26	83.9	456	1 KICH_HUMAN	P35790 homo sapien
36	26	83.9	1407	1 CYAA_DICDI	Q03100 dictyosteli
37	26	83.9	2017	1 MYSN_DROME	Q99323 drosophila
38	25	80.6	259	1 FLA2_NATMA	O93718 natrialba m
39	25	80.6	295	1 PYRB_CAMJE	O99j16 campylobact
40	25	80.6	313	1 CDX2_HUMAN	O99626 homo sapien
41	25	80.6	313	1 CDX2_MESAU	O04649 mesocricetu
42	25	80.6	334	1 CHM1_RAT	O70367 rattus norv
43	25	80.6	362	1 ALEU_HORVU	P05167 hordeum vul
44	25	80.6	397	1 AAT_STRVG	O60013 streptomyce
45	25	80.6	426	1 HISX_METTH	O26327 methanobact

ALIGNMENTS

RESULT 1					
ID	KV3P_MOUSE	STANDARD;	PRT;	110 AA.	
AC	P01668;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V-III region PC 7210.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=79073152; PubMed=103003;				
RA	Wiegert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;				
RT	"Rearrangement of genetic information may produce immunoglobulin				
RT	diversity."				
RL	Nature 276:785-790(1978).				
DR	PIR; D01937; KVM510.				
DR	HSSP; P01679; 2FBJ.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	PIfam; PF00047; Ig; 1.				
DR	SMART; SM00406; IgV; 1.				
KW	Immunoglobulin V region.				
FT	DOMAIN 1 23				FRAMEWORK-1.
FT	DOMAIN 24 38				COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 29 53				FRAMEWORK-2.
FT	DOMAIN 54 60				COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 61 92				FRAMEWORK-3.
FT	DOMAIN 93 100				COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN 101 110				FRAMEWORK-4.
FT	DISULFID 23 92				BY SIMILARITY.
FT	NON_TER 110 110				
SQ	SEQUENCE 110 AA; 11950 MW; 69FIA5CE86B1249 CRC64;				
Query Match 100.0%; Score 31; DB 1; Length 110;					
Best Local Similarity 100.0%; Pred. No. 0.86;					
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 AASNLES 7				
Db	54 AASNLES 60				
RESULT 2					
ID	KV3L_MOUSE	STANDARD;	PRT;	111 AA.	
AC	P01664;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V-III region CBPC 101.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

Query Match	100.0%;	Score 31;	DB 1;	Length 111;
Best Local Similarity	100.0%;	Pred. No. 0.87;		
Matches	7;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	AASNLES 7		
Db	54	AASNLES 60		
RESULT 4				
KV3N_MOUSE		STANDARD;	PRT;	111 AA.
ID	KV3N_MOUSE			
AC	P01686;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-III region PC 7183.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=79073152; PubMed=103003;			
RA	Weigert M., Gattaitan L., Loh E., Schilling J., Hood L.E.;			
RT	"Rearrangement of genetic information may produce immunoglobulin			
RT	diversity."			
RL	Nature 276:785-790(1978).			
RL	PIR: B01937; KVM883.			
DR	HSP: P01679; 2FBJ.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; Ig: 1.			
DR	SMART; SM00406; IGV; 1.			
KW	Immunoglobulin V region.			
FT	DOMAIN 1 23			
FT	DOMAIN 24 38			
FT	DOMAIN 39 53			
FT	DOMAIN 54 60			
FT	DOMAIN 61 92			
FT	DOMAIN 93 101			
FT	DOMAIN 102 111			
FT	DISULFID 23 92			
FT	NON_TER 111 111			
SQ	SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;			
Query Match	100.0%;	Score 31;	DB 1;	Length 111;
Best Local Similarity	100.0%;	Pred. No. 0.87;		
Matches	7;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	AASNLES 7		
Db	54	AASNLES 60		
RESULT 5				
KV3Q_MOUSE		STANDARD;	PRT;	111 AA.
ID	KV3Q_MOUSE			
AC	P01669;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-III region PC 7769.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=79073152; PubMed=103003;			
RA	Weigert M., Gattaitan L., Loh E., Schilling J., Hood L.E.;			
RT	"Rearrangement of genetic information may produce immunoglobulin			

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RT diversity";
RL Nature 276:785-790(1978).
DR PIR; E01937; KMS69.
DR HSP; F80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.87; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 AASNLES 7
DB 54 AASNLES 60

RESULT 6
ID YIEO_HAEIN STANDARD; PRT; 463 AA.
AC P44903;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical transport protein HI0852.
GN HI0852.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Rd / KW20 / ATCC 51907;
RC MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Frichman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
RL Science 269:496-512(1995).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (probable).
CC -!- SIMILARITY: STRONG, TO E.COLI YIEO.
CC -!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
CC -----
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CC -----
CC EMBL; U32766; AAC22509.1; -.

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DR TIGR; HI0852; -.
DR InterPro; IPR004638; Efflux_EmrB.
DR InterPro; IPR003662; sub_transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR TIGRFAMS; TIGR00711; efflux_EmrB; 1.
KW Hypothetical protein; Transport; Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 49 69 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 107 127 POTENTIAL.
FT TRANSMEM 139 159 POTENTIAL.
FT TRANSMEM 165 185 POTENTIAL.
FT TRANSMEM 197 217 POTENTIAL.
FT TRANSMEM 225 245 POTENTIAL.
FT TRANSMEM 267 287 POTENTIAL.
FT TRANSMEM 298 318 POTENTIAL.
FT TRANSMEM 328 348 POTENTIAL.
FT TRANSMEM 354 374 POTENTIAL.
FT TRANSMEM 393 413 POTENTIAL.
FT TRANSMEM 429 449 POTENTIAL.
SQ SEQUENCE 463 AA; 50002 MW; D725EPFD50F9P23F CRC64;

Query Match 100.0%; Score 31; DB 1; Length 463;
Best Local Similarity 100.0%; Pred. No. 4.2; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 AASNLES 7
DB 94 AASNLES 100

RESULT 7
ID KVIG_HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RA "The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), I. The amino acid sequence of the L-chain of kappa-type subgroup 1.";
RA Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
CC PIR; A01867; K1HUGL.
CC HSP; P01607; IREI.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

```

Query Match 90.3%; Score 28; DB 1; Length 108;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
| | | | | : |
DB 50 AASNL5 56

RESULT 8
VP9_WTV
ID VP9_WTV STANDARD; PRT; 313 AA.
AC P12326;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Structural protein P9 (Capsomere protein P9) (Protein PNS11).
GN S11.
OS Wound tumor virus (WTV).
OC Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.
OX NCBI_TaxID=10987;

[1]
SEQUENCE FROM N.A.
RA MEDLINE=89263810; PubMed=2726499;
RA Dall D.J., Anzola J.V., Xu Z., Nuss D.L.;
RT "Complete nucleotide sequence of wound tumor virus genomic segment
S11."
RL Nucleic Acids Res. 17:3599-3599(1989).
CC -!- SIMILARITY: TO RICE DWARF VIRUS S9 AND RICE GALL DWARF VIRUS S10.
CC
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CC
CC EMBL; X14219; CAA32439.1; -
DR PIR; S04139; QMXRW.
SQ SEQUENCE 313 AA; 35606 MW; 6746F59840AD17F2 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 313;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
| | | | | : |
DB 294 AASNL5 300

RESULT 9
VP9_WTVNJ
ID VP9_WTVNJ STANDARD; PRT; 313 AA.
AC P31611;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Structural protein P9 (Capsomere protein P9) (Protein PNS11).
OS Wound tumor virus (strain NJ) (WTV).
OC Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.
OX NCBI_TaxID=31595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92074261; PubMed=1962460;
RA Hillman B.I., Anzola J.V., Halpern B.T., Cavilleer T.D., Nuss D.L.;
RT "First field isolation of wound tumor virus from a plant host:
RT minimal sequence divergence from the type strain isolated from an
RT insect vector."
RL Virology 185:896-900(1991).
CC -!- SIMILARITY: TO RICE DWARF VIRUS S9 AND RICE GALL DWARF VIRUS S10.
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CC
CC EMBL; M77020; AAA48500.1; -
DR PIR; C41705; QMXRW.
KW Nonstructural protein.

SQ SEQUENCE 313 AA; 35551 MW; D9B904785C601C34 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 313;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
| | | | | : |
DB 294 AASNL5 300

RESULT 10
FTSH_HELPJ
ID FTSH_HELPJ STANDARD; PRT; 632 AA.
AC Q9ZM66;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cell division protein ftsh homolog (EC 3.4.24.-).
GN FTSH OR JHP0356.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
CC -!- FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE
CC (BY SIMILARITY).
CC -!- COFACTOR: BINDS 1 ZINC ION (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41.

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CC
CC EMBL; AE001471; AAD05932.1; -
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_cent.
DR InterPro; IPR003960; AAA_sub.
DR InterPro; IPR000642; Peptidase_M41.
DR Pfam; PF00004; AAA_1.
DR Pfam; PF01434; Peptidase_M41; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR01241; FtsH_fam; 1.
DR PROSITE; PS00674; AAA; 1.
DR Cell division; ATP-binding; Transmembrane; Hydrolase; Metalloprotease;
KW Zinc; Complete proteome.
FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 10 31 POTENTIAL.
 FT DOMAIN 32 116 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 117 137 POTENTIAL.
 FT DOMAIN 138 632 CYTOPLASMIC (POTENTIAL).
 FT NP_BIND 210 217 ATP (POTENTIAL).
 FT METAL 434 434 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 435 435 BY SIMILARITY.
 FT METAL 438 438 ZINC (CATALYTIC) (BY SIMILARITY).
 SQ SEQUENCE 632 AA; 69765 MW; 2FB67B43C51559FB CRC64;

Query Match 90.3%; Score 28; DB 1; Length 632;
 Best Local Similarity 85.7%; Pred. No. 33;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 |||:||||
 Db 616 AASNLES 622

RESULT 11
 KL68_DROME STANDARD; PRT; 784 AA.
 AC F46867; Q9VTN8;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kinesin-like protein, KLP68D.
 GN KLP68D OR KLP5 OR CG7293.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95050960; PubMed=7525600;
 RA Pesavento P.A., Stewart R.J., Goldstein L.S.B.;
 RT "Characterization of the KLP68D kinesin-like protein in Drosophila:
 RT possible roles in axonal transport.";
 RL J. Cell Biol. 127:1041-1048(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkuch C., Baldwin D.,
 RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimball B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 [3]
 RP SEQUENCE OF 220-342 FROM N.A.
 RX MEDLINE=92020874; PubMed=1924306;
 RA Stewart R.J., Pesavento P.A., Woerpel D.N., Goldstein L.S.B.;
 RT "Identification and partial characterization of six members of the
 RT kinesin superfamily in Drosophila";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8470-8474(1991).
 CC -!- FUNCTION: PLUS-END DIRECTED MICROTUBULE MOTOR THAT MAY BE USED FOR
 CC ANTEROGRADE AXONAL TRANSPORT AND COULD CONCEIVABLY MOVE CARGOES IN
 CC FLY NEURONS DIFFERENT THAN THOSE MOVED BY KINESIN HEAVY CHAIN OR
 CC OTHER PLUS-END DIRECTED MOTORS.
 CC -!- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE CENTRAL NERVOUS
 CC SYSTEM AND IN A SUBSET OF THE PERIPHERAL NERVOUS SYSTEM DURING
 CC EMBRYOGENESIS.
 CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
 CC II SUBFAMILY.
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 DR EMBL; U15974; AAA69929.1; -;
 DR EMBL; M74431; AAA28658.1; -;
 DR EMBL; AE003543; AAF50008.1; -;
 DR HSSP; P17119; 3KAR.
 DR FlyBase; FBgn004381; Klp68D.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; P50041; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE; P50067; KINESIN_MOTOR_DOMAIN2; 1.
 KW Motor protein; Microtubules; ATP-binding; Coiled coil.
 FT DOMAIN 16 275 KINESIN-MOTOR.
 FT DOMAIN 351 385 COILED COIL (POTENTIAL).
 FT DOMAIN 426 582 COILED COIL (POTENTIAL).
 FT NP_BIND 106 113 ATP (POTENTIAL).
 FT CONFLICT 220 221 SS -> TC (IN REF. 3).
 FT CONFLICT 338 342 GSRAK -> VRGOV (IN REF. 3).
 FT CONFLICT 338 338 G -> A (IN REF. 2).
 SQ SEQUENCE 784 AA; 88193 MW; 94BB9BADF072DFC0 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 784;
 Best Local Similarity 85.7%; Pred. No. 42;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 |||||:
 Db 751 AASNLES 757

RESULT 12
 KV1B_HUMAN STANDARD; PRT; 108 AA.
 ID KV1B_HUMAN
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-1 region AU.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 protein Au).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 Bence-Jones protein Au.";
 RL Biophys. Struct. Mech. 1:139-146(1975).
 CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 REGION OF THE KAPPA CHAIN REI.
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01862; KIHUAA.
 DR HSSP: P01607; IREI.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E8011187E56F6B9 CRC64;
 Query Match 87.1%; Score 27; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ASNLES 7
 DB 51 ASNLES 56
 RESULT 13
 KV3V_MOUSE
 ID KV3V_MOUSE STANDARD; PRT; 108 AA.
 AC P01674;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 2154.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Ioh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: A01940; KVM54.
 DR HSSP: P80362; LWTL.
 DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 108
 FT DISULFID 23 92
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11699 MW; D40921D18DAC4B9E CRC64;
 Query Match 87.1%; Score 27; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ASNLES 7
 DB 55 ASNLES 60
 RESULT 14
 KV3H_MOUSE
 ID KV3H_MOUSE STANDARD; PRT; 111 AA.
 AC P01660;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 3741/TEPC 111.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE (PC 3741).
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Ioh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 RN [2]
 RP SEQUENCE (TEPC 111).
 RX MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 related mouse kappa variable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 CC -!- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
 DR PIR: A01934; KVM537.
 DR HSSP: P01679; 2FBJ.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;
 Query Match 87.1%; Score 27; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 8.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASNLES 7
 Db 55 ASNLES 60

RESULT 15
 KV3J_MOUSE
 ID KV3J_MOUSE STANDARD; PRT; 111 AA.
 AC P01662;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region ABPC 22/PC 9245.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 SEQUENCE (ABPC 22).
 MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 RT related mouse kappa variable regions";
 RN Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 RN [2]
 SEQUENCE (PC 9245).
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity";
 RN Nature 276:785-790(1978).
 CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
 DR PIR; A01935; KVM56.
 DR HSP; P01679; 2FEU.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 87.1%; Score 27; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 8.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASNLES 7
 Db 55 ASNLES 60

Search completed: February 14, 2003, 11:16:23
 Job time : 4.6129 secs

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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:10:17 ; Search time 14.5645 Seconds
(without alignments)
99.030 Million cell updates/sec

Title: US-09-701-001B-5
Perfect score: 31
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL 21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhch.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	31	100.0	508	4	Q96RS9	Q96RS9 homo sapien
2	31	100.0	942	3	O42938	O42938 schizosacch
3	31	100.0	1208	4	O75162	O75162 homo sapien
4	28	90.3	69	16	Q8YFL0	Q8YFL0 bruceella me
5	28	90.3	103	11	Q9JL80	Q9JL80 mus musculus
6	28	90.3	204	5	Q9U2Y4	Q9U2Y4 caenorhabdi
7	28	90.3	209	16	Q9A698	Q9A698 caulobacter
8	28	90.3	228	16	Q8U760	Q8U760 agrobacteri
9	28	90.3	302	10	Q9ATD5	Q9ATD5 gossypium h
10	28	90.3	579	16	Q8YSW1	Q8YSW1 anabaena sp
11	28	90.3	784	5	Q961H5	Q961H5 drosophila
12	27	87.1	111	11	Q920E9	Q920E9 mus musculu
13	27	87.1	310	16	P94981	P94981 mycobacteri
14	27	87.1	326	16	Q8YEF7	Q8YEF7 bruceella me
15	27	87.1	389	10	Q9SAF7	Q9SAF7 arabidopsis
16	27	87.1	419	10	Q9M887	Q9M887 arabidopsis

17	27	87.1	443	10	Q9LI76	Q9LI76 arabidopsis
18	27	87.1	468	10	Q9ASW0	Q9ASW0 arabidopsis
19	27	87.1	468	10	Q9LFX3	Q9LFX3 arabidopsis
20	27	87.1	497	3	O74901	O74901 schizosacch
21	27	87.1	510	16	Q9A8L5	Q9A8L5 caulobacter
22	27	87.1	517	3	Q9C128	Q9C128 pichia past
23	27	87.1	576	12	Q9JGJ9	Q9JGJ9 soil-borne
24	27	87.1	619	2	Q9F9H4	Q9F9H4 rickettsia
25	27	87.1	643	10	Q9LSX2	Q9LSX2 arabidopsis
26	27	87.1	678	5	Q8WR60	Q8WR60 drosophila
27	27	87.1	689	17	Q9HMT9	Q9HMT9 halobacteri
28	27	87.1	746	3	Q08754	Q08754 saccharomyc
29	27	87.1	826	13	Q9YHD5	Q9YHD5 rana catesb
30	27	87.1	829	16	Q8YQK8	Q8YQK8 anabaena sp
31	27	87.1	856	5	Q9V706	Q9V706 drosophila
32	27	87.1	927	16	Q9PGG3	Q9PGG3 xylella fas
33	27	87.1	1195	13	Q9PUM2	Q9PUM2 xenopus lae
34	27	87.1	1425	2	O85862	O85862 sphingomona
35	27	87.1	2406	5	Q9N905	Q9N905 trypanosoma
36	27	87.1	5085	11	Q9JKS6	Q9JKS6 rattus norv
37	26	83.9	173	16	Q8YTF5	Q8YTF5 anabaena sp
38	26	83.9	297	16	O50805	O50805 borrelia bu
39	26	83.9	327	10	Q8RYK6	Q8RYK6 oryza sativ
40	26	83.9	367	10	Q9SE32	Q9SE32 oryza sativ
41	26	83.9	367	10	Q9FPB1	Q9FPB1 oryza sativ
42	26	83.9	373	10	Q8W516	Q8W516 hordeum vul
43	26	83.9	408	4	O94798	O94798 homo sapien
44	26	83.9	435	11	Q91VI8	Q91VI8 mus musculu
45	26	83.9	444	4	Q9UHX4	Q9UHX4 homo sapien

ALIGNMENTS

RESULT 1

Q96RS9	PRELIMINARY;	PRT;	508 AA.
ID	Q96RS9		
AC	Q96RS9;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	DZIP3 (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Moore F.L., Reijo R.A.;		
RT	"Novel DZIP3 Protein Interacts with DAZ Protein."		
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF279370; AAK69484.1; -		
FT	NON_TER 1		
SQ	SEQUENCE 508 AA; 57962 MW; EF2C079B1A1CF22 CRC64;		

Query Match 100.0%; Score 31; DB 4; Length 508;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 256 AASNLES 262

RESULT 2

O42938	PRELIMINARY;	PRT;	942 AA.
ID	O42938		
AC	O42938;		
DT	01-JUN-1998 (TrEMBLrel. 06, Created)		
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	Probable 6-phosphofructokinase beta subunit (EC 2.7.1.11)		
DE	(Phosphofructokinase 1) (Phosphohexokinase) (6PF-1-K beta subunit).		

```

GN SPBC16H5.02.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: ATP + D-FRUCTOSE 6-PHOSPHATE = ADP + D-
CC FRUCTOSE 1,6-BISPHOSPHATE.
CC -|- PATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.
CC -|- SUBUNIT: HETEROCTAMER OF 4 ALPHA AND 4 BETA CHAINS (BY
CC SIMILARITY).
DR EMBL; AL022104; CAA17900.1; -.
DR HSSP; P00512; 3PFK.
DR InterPro; IPR000023; Ppfuckinase.
DR Pfam; PF00365; PFK; 2.
DR PRINTS; PR00476; PHFRCTKINASE.
DR PRODOM; PD000707; Ppfuckinase; 2.
DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 2.
KW Kinase; Transferase; Glycolysis; Repeat; Allosteric enzyme;
KW Phosphorylation; Magnesium.
SQ SEQUENCE 942 AA; 102554 MW; C6052AF7C1DB75B4 CRC64;

Query Match 100.0%; Score 31; DB 3; Length 942;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 165 AASNLES 171
|||||

RESULT 3
ID O75162 PRELIMINARY; PRT; 1208 AA.
AC O75162;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE KIAA0675 protein.
GN KIAA0675.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RC MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
CC -|- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AB014575; BAA31650.1; -.
DR HSSP; P28990; ICHC.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 1208 AA; 138604 MW; 76945A63AF85207E CRC64;

Query Match 100.0%; Score 31; DB 4; Length 1208;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

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Db 896 AASNLES 902
|||||

RESULT 4
Q8YFLO PRELIMINARY; PRT; 69 AA.
ID Q8YFLO;
AC Q8YFLO;
DT 01-WAR-2002 (TREMBLrel. 20, Created)
DT 01-WAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cold shock protein CSPa.
GN BMEI1510.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
RC MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mijer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyripides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009587; AAL52691.1; -.
DR InterPro; IPR002059; Cold_shock.
DR Pfam; PF00313; CSD; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR PRODOM; PD000621; Cold_shock; 1.
DR SMART; SM00357; CSP; 1.
DR PROSITE; PS00352; COLD_SHOCK; 1.
KW Complete proteome.
SQ SEQUENCE 69 AA; 7301 MW; D6142414631FEDEBA CRC64;

Query Match 90.3%; Score 28; DB 16; Length 69;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 62 AASNLES 68
|||||

RESULT 5
Q9JL80 PRELIMINARY; PRT; 103 AA.
ID Q9JL80;
AC Q9JL80;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RC MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206026; AAF69324.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.

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DR InterPro: IPR003596; Iq_v.

DR Pfam: PF00047; Iq; 1.

DR SMART: SM00406; IGV; 1.

FT NON_TER 103

FT NON_TER 103

SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

Query Match 90.3%; Score 28; DB 11; Length 103;

Best Local Similarity 85.7%; Pred. No. 25;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 46 AASNLES 52

RESULT 6

Q902Y4

Q902Y4 PRELIMINARY; PRT; 204 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE Y113G7A.14 protein.

GN Y113G7A.14

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OC NCBI_TaxID=6239;

OX [1]

RN SEQUENCE FROM N.A.

RP Lennard N.

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99059613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for

investigating biology";

RL Science 282:2012-2018(1998).

RL EMBL; ALI32858; CAB60484.1; -.

SQ SEQUENCE 204 AA; 23067 MW; 8968065DF2EA9C7E CRC64;

Query Match 90.3%; Score 28; DB 5; Length 204;

Best Local Similarity 85.7%; Pred. No. 52;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 134 AASNLES 140

RESULT 7

Q9A698

Q9A698 PRELIMINARY; PRT; 209 AA.

AC Q9A698;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Hypothetical protein CC2196.

GN CC2196.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;

OC Caulobacter.

OC NCBI_TaxID=155892;

RN [1]

RP SEQUENCE FROM N.A.

RP STRAIN=ATCC 19089 / CB15;

RX MEDLINE=21173698; PubMed=11259647;

RA Niernan W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
FT "Complete genome sequence of *Caulobacter crescentus*.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RL EMBL; AE005891; AAK24167.1; -.
RW TIGR; CC2196; -.
KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 209 AA; 22181 MW; D02002477F7E9E2D CRC64;

Query Match 90.3%; Score 28; DB 16; Length 209;

Best Local Similarity 85.7%; Pred. No. 53;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 151 AASNLES 157

RESULT 8

Q8U760

Q8U760 PRELIMINARY; PRT; 228 AA.

AC Q8U760;

DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Hypothetical protein Atu4594.

GN ATU4594 OR AGR.L.563.

OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Rhizobium.

OC NCBI_TaxID=176299;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21608550; PubMed=11743193;

RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

RA Kutayin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

RA Nester E.W.;

RT "The genome of the natural genetic engineer *Agrobacterium tumefaciens*

C58.";

RT Science 294:2317-2323(2001).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21608551; PubMed=11743194;

RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,

RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,

RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,

RA Cielo C., Slater S.;

RT "Genome sequence of the plant pathogen and biotechnology agent

Agrobacterium tumefaciens C58.";

RT Science 294:2323-2328(2001).

DR EMBL; AE009387; AAL45388.1; -.

DR EMBL; AE008228; AAK88851.1; -.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 228 AA; 24816 MW; 4B03E65F8F8A998 CRC64;

Query Match 90.3%; Score 28; DB 16; Length 228;

Best Local Similarity 85.7%; Pred. No. 58;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 156 AASNLES 162

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RESULT 9
Q9ATD5
ID Q9ATD5 PRELIMINARY; PRT; 302 AA.
AC Q9ATD5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE GHVYB10.
GN GHVYB10.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ACALA MAXXA; TISSUE=DAY OF ANTHESIS OVULE;
RA Matz E.C., Burr B.;
RT "Cotton seed fibers are trichomes.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL: AF336282; AAK19615.1; -.
DR HSP; P06876; 1MBK.
DR InterPro; IPR001005; Myb_DNA_binding.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
DR DNA-binding; Nuclear protein.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 302 AA; 33816 MW; 48EE5D9D921ED2D7 CRC64;

Query Match 90.3%; Score 28; DB 10; Length 302;
Best Local Similarity 85.7%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 286 AASNLSQ 292

RESULT 10
Q8YSW1
ID Q8YSW1 PRELIMINARY; PRT; 579 AA.
AC Q8YSW1;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein ALI2969.
GN ALI2969.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003591; BAB74668.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 579 AA; 66557 MW; 5C00EBD8CF31BB97 CRC64;

Query Match 90.3%; Score 28; DB 16; Length 579;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AASNLES 7
Db 378 AASNLS 384

RESULT 11
Q961H5
ID Q961H5 PRELIMINARY; PRT; 784 AA.
AC Q961H5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE GH23075p.
GN KLP68D OR CG7293.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celnik S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY051583; AAK93007.1; -.
DR FlyBase; FBgn0004381; Klp68D.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Coiled coil; Microtubules; Motor protein.
SQ SEQUENCE 784 AA; 88207 MW; 7A3C6716D22BC05D CRC64;

Query Match 90.3%; Score 28; DB 5; Length 784;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 751 AASNLS 757

RESULT 12
Q920E9
ID Q920E9 PRELIMINARY; PRT; 111 AA.
AC Q920E9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307935; AAL09419.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 12046 MW; 1B46988AA6858526 CRC64;
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Query Match 87.1%; Score 27; DB 11; Length 111;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 |||||
 DB 55 ASNLES 60

RESULT 13
 P94981 ID P94981 PRELIMINARY; PRT; 310 AA.
 AC P94981;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 30.2 kDa protein (PE family protein).
 GV RV1646 OR MFCY06H11.11 OR MT1684.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / OSHKOSH;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z85982; CAB06640.1; -;
 DR EMBL; AE007031; AAK45953.1; -;
 DR TIGR; MT1684; -;
 DR TubercuList; Rv1646; -;
 DR InterPro: IPR000084; PE_region.
 DR Pfam; PF00934; PE; 1.
 DR ProDom; PD001223; PE_region; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 310 AA; 30219 MW; F51DFE4CC2D9EDAD CRC64;

Query Match 87.1%; Score 27; DB 16; Length 310;
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AASNLES 7
 |||||
 DB 14 AAGNLES 20

RESULT 14
 Q8YEF7 ID Q8YEF7 PRELIMINARY; PRT; 326 AA.
 AC Q8YEF7;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Acetoacetyl-CoA synthetase (EC 6.2.1.16).
 GN BME11921.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kapratral V., Redkar R.J., Patra G., Mijer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyrides N., Overbeek R.;
 RA "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL; AE009625; AAL53102.1; -;
 DR InterPro: IPR000873; AMP-bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR PROSITE; PS00455; AMP_BINDING; 1.
 KW Ligase; Complete proteome.
 SQ SEQUENCE 326 AA; 36286 MW; 2092FC153E63A80C CRC64;

Query Match 87.1%; Score 27; DB 16; Length 326;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLE 6
 |||||
 DB 25 AASNLE 30

RESULT 15
 Q9SAF7 ID Q9SAF7 PRELIMINARY; PRT; 389 AA.
 AC Q9SAF7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE F3F19.26 protein.
 GN F3F19.26.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lee J.M., Lenz C.,
 RA Liu S., Li J., Kremenetskaia I., Luros J., Ngan I., Gonzalez A.,
 RA Altafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P.,
 RA Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
 RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
 RT "Arabidopsis thaliana chromosome 1 BAC F3F19 sequence."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Theologis A.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC007357; AAD31076.1; -;
 DR InterPro: IPR001360; GH_1.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003592; LRR_out.
 DR Pfam; PF00560; LRR; 8.
 DR PRINTS; PR00019; LEURICRPT.
 DR SMART; SM00370; LRR; 7.
 DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_1.
 SQ SEQUENCE 389 AA; 43216 MW; 1DC342A0BF4B7EBF CRC64;

Query Match 87.1%; Score 27; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
|
|
|
|
|
|
Db 106 ASNLES 111

Search completed: February 14, 2003, 11:18:43
Job time : 16.7312 secs

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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:04:17 ; Search time 24.3871 Seconds
(without alignments)
49.176 Million cell updates/sec

Title: US-09-701-001B-6
Perfect score: 48
Sequence: 1 QOSSEDPPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

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17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	9	AAV59261	Antibody 4H5 L cha
2	48	100.0	9	AAV51138	Murine CD4/CD34 re
3	48	100.0	103	AAV59263	Antibody 4H5 L cha
4	48	100.0	103	AAV51140	Murine derived pro
5	48	100.0	111	AAV59267	Antibody 4H5 L cha
6	48	100.0	111	AAV51144	Murine derived pro
7	48	100.0	111	AAV51146	Murine derived pro
8	48	100.0	131	AAV32123	Anti-CD4 antibody
9	48	100.0	305	AAV59264	Antibody 4H5 H cha
10	48	100.0	305	AAV59265	Antibody 4H5 L cha

11	48	100.0	305	21	AAV51141	Murine derived pro
12	48	100.0	305	21	AAV51142	Murine derived pro
13	45	93.8	9	16	AAV70197	MAB 3B9 light chai
14	45	93.8	9	20	AAV23774	CDR of the light c
15	45	93.8	9	20	AAV18116	Light chain CDR fo
16	45	93.8	111	20	AAV23781	Light chain variab
17	45	93.8	111	20	AAV18123	Light chain sequen
18	45	93.8	131	13	AAV29008	p64-k4 protein pro
19	45	93.8	131	16	AAV70202	Humanized antibody
20	45	93.8	131	18	AAV30274	Light chain of Hum
21	45	93.8	131	18	AAV30278	Light chain of Mum
22	45	93.8	131	20	AAV23779	Light chain variab
23	45	93.8	131	20	AAV18126	Light chain sequen
24	45	93.8	132	16	AAV70189	Mouse MAB 3B9 ligh
25	45	93.8	132	20	AAV23767	Light chain variab
26	45	93.8	132	20	AAV18120	Light chain sequen
27	42	87.5	17	15	AAV66145	CD-4 antibody vari
28	42	87.5	115	11	AAV04134	Anti-Leu 3a light
29	42	87.5	131	11	AAV04132	Anti-Leu 3a light
30	40	83.3	9	16	AAV70201	Humanized antibody
31	40	83.3	9	20	AAV23778	CDR of the light c
32	40	83.3	9	20	AAV18119	Light chain CDR fo
33	40	83.3	10	23	AAV70354	Mouse kappa III li
34	40	83.3	131	16	AAV75355	Humanized antibody
35	40	83.3	131	20	AAV23771	Light chain variab
36	40	83.3	131	20	AAV18118	Light chain sequen
37	38	79.2	282	21	AAV41486	Arabidopsis thalia
38	38	79.2	301	21	AAV41485	Arabidopsis thalia
39	38	79.2	304	22	AAV02541	A. thaliana transc
40	38	79.2	304	23	AAV02594	Arabidopsis transc
41	38	79.2	318	21	AAV41484	Arabidopsis thalia
42	37	77.1	215	16	AAV64202	Monoclonal antibod
43	37	77.1	495	21	AAV29957	Arabidopsis thalia
44	37	77.1	513	21	AAV29956	Arabidopsis thalia
45	37	77.1	517	21	AAV29955	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAV59261
ID AAV59261 standard; peptide; 9 AA.
XX AAV59261;
XX
DT 17-APR-2000 (first entry)
XX
DE Antibody 4H5 L chain variable region CDR3 fragment.
DE
KW CD4 antigen; anti-human; antibody; 4H5; drug; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN JP11332563-A.
XX
PD 07-DEC-1999.
XX
PF 26-MAY-1998; 98JP-0163034.
XX
PR 26-MAY-1998; 98JP-0163034.
XX
PA (ASAH) ASAH KASEI KOGYO KK.
XX
DR WPI; 2000-091351/08.
PT An antibody and the nucleic acid coding the antibody -
XX
PS Claim 2; Page 14; 25pp; Japanese.
XX
CC The invention provides an antibody having affinity to CD4 antigen. The
anti-human CD4 antibody 4H5 is used for the detection of antigen and

CC application for drugs. It is highly safe in human dose. Sequences
CC AAY59259-61 represent the complementarity determining region (CDR)-1,
CC CDR-2 and CDR-3 fragments in the L chain variable region of the
CC antibody 4H5 respectively.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
| | | | | | | | | |
DB 1 QOSSEDPPT 9

RESULT 2
AAY51138
ID AAY51138 standard; Protein; 9 AA.
XX
AC AAY51138;
XX
DT 31-MAR-2000 (first entry)
XX
DE Murine CD4/CD34 recognizing antibody light chain CDR-3 region #1.
XX
KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; complementarity determining region;
KW CDR-3; light chain; murine.
XX
OS Mus sp.
XX
PN WO9961629-A1.
XX
PD 02-DEC-1999.
XX
PF 24-MAY-1999; 99WO-JP02711.
XX
PR 25-MAY-1998; 98JP-0159957.
XX
PR 26-MAY-1998; 98JP-0163023.
XX
XX (ASAH) ASAH KASEI KOGYO KK.
PA (ASAH) ASAH MEDICAL CO LTD.
XX
PI Ono M, Soka T, Morimoto I, Miyamura K;
XX
DR WPI; 2000-086720/07.
XX
PS Devices containing antibodies recognising CD4 or CD34 and their use for
XX the separation of CD4 or CD34 positive cells -
XX
PS Claim 3; Page 77; 11pp; Japanese.
XX
CC This invention describes a novel device (1) for separating cluster
CC differentiation (CD)-positive cells using a recombinant (chimeric or
CC single-chain) antibody recognising CD4 or CD34. The devices are useful
CC for the separation of CD4 or CD34 positive cells, which is useful for
CC the collection of hematopoietic undifferentiated cells, elimination of
CC lymphocytes from cells to be used in bone marrow transplantation, the
CC detection of leukemic cells and the production of medicinal
CC compositions for the treatment of HIV infection and autoimmune diseases.
CC This sequence represents a murine derived complementarity determining
CC region CDR-3 protein fragment which is used to illustrate the method of
CC the invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9

DB 1 QOSSEDPPT 9
| | | | | | | | | |
RESULT 3
AAY59263
ID AAY59263 standard; protein; 103 AA.
XX
AC AAY59263;
XX
DT 17-APR-2000 (first entry)
XX
DE Antibody 4H5 L chain variable region.
XX
KW CD4 antigen; anti-human; antibody; 4H5; drug.
XX
OS Mus sp.
XX
PN JP11332563-A.
XX
PD 07-DEC-1999.
XX
PF 26-MAY-1998; 98JP-0163034.
XX
PR 26-MAY-1998; 98JP-0163034.
XX
XX (ASAH) ASAH KASEI KOGYO KK.
PA WPI; 2000-091351/08.
XX
DR N-PSDB; AAZ58662.
XX
PT An antibody and the nucleic acid coding the antibody -
XX
PS Claim 5; Page 15-16; 25pp; Japanese.
XX
CC The invention provides an antibody having affinity to CD4 antigen. The
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
CC application for drugs. It is highly safe in human dose. The present
CC sequence represents the L chain variable region of the antibody 4H5.
XX
SQ Sequence 103 AA;

Query Match 100.0%; Score 48; DB 21; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
| | | | | | | | | |
DB 85 QOSSEDPPT 93

RESULT 4
AAY51140
ID AAY51140 standard; Protein; 103 AA.
XX
AC AAY51140;
XX
DT 31-MAR-2000 (first entry)
XX
DE Murine derived protein fragment #2.
XX
KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; murine.
XX
OS Mus sp.
XX
PN WO9961629-A1.
XX
PD 02-DEC-1999.
XX
PF 24-MAY-1999; 99WO-JP02711.
XX

PR 25-MAY-1998; 98JP-0159957.
 PR 26-MAY-1998; 98JP-0163023.
 XX
 XX (ASAH) ASAHI KASEI KOGYO KK.
 XX (ASAH) ASAHI MEDICAL CO LTD.
 XX
 XX PI Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI; 2000-086720/07.
 DR N-PSDB; AA244204.
 XX
 XX Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells -
 XX
 XX Claim 22; Page 79; 111pp; Japanese.
 XX
 XX This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 XX
 XX SQ Sequence 103 AA;
 Query Match 100.0%; Score 48; DB 21; Length 103;
 Best Local Similarity 100.0%; Pred. No. 0.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QOSSEDPPT 9
 Db 85 QOSSEDPPT 93
 |||||
 RESULT 5
 AAY59267
 ID AAY59267 standard; protein; 111 AA.
 XX
 XX AAY59267;
 XX
 XX 17-APR-2000 (first entry)
 DT
 XX Antibody 4H5 L chain fragment.
 XX
 XX CD4 antigen; anti-human; antibody; 4H5; drug.
 KW
 XX Mus sp.
 OS
 XX JP11332563-A.
 PN
 XX 07-DEC-1999.
 PD
 XX 26-MAY-1998; 98JP-0163034.
 PF
 XX 26-MAY-1998; 98JP-0163034.
 PR
 XX (ASAH) ASAHI KASEI KOGYO KK.
 XX
 XX WPI; 2000-091351/08.
 DR N-PSDB; AA258690.
 DR
 XX An antibody and the nucleic acid coding the antibody -
 PT
 XX Disclosure; Page 22-23; 25pp; Japanese.
 PS
 XX The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents a L chain fragment of the antibody 4H5.

XX SQ Sequence 111 AA;
 Query Match 100.0%; Score 48; DB 21; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.64;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QOSSEDPPT 9
 Db 93 QOSSEDPPT 101
 |||||
 RESULT 6
 AAY51144
 ID AAY51144 standard; Protein; 111 AA.
 XX
 XX AAY51144;
 AC
 XX 31-MAR-2000 (first entry)
 DT
 XX Murine derived protein fragment #6.
 DE
 XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 XX
 XX Mus sp.
 OS
 XX WO9961629-A1.
 PN
 XX 02-DEC-1999.
 PD
 XX 24-MAY-1999; 99WO-JP02711.
 PF
 XX 25-MAY-1998; 98JP-0159957.
 PR
 XX 26-MAY-1998; 98JP-0163023.
 PR
 XX (ASAH) ASAHI KASEI KOGYO KK.
 XX (ASAH) ASAHI MEDICAL CO LTD.
 PA
 XX Ono M, Soka T, Morimoto I, Miyamura K;
 PI WPI; 2000-086720/07.
 DR
 XX Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells -
 XX
 XX Disclosure; Page 95; 111pp; Japanese.
 PS
 XX This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 XX
 XX SQ Sequence 111 AA;
 Query Match 100.0%; Score 48; DB 21; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.64;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QOSSEDPPT 9
 Db 93 QOSSEDPPT 101
 |||||
 RESULT 7
 AAY51146

ID AAY51146 standard; Protein; 111 AA.
 XX AAY51146;
 AC
 XX 31-MAR-2000 (first entry)
 DT
 XX Murine derived protein fragment #8.
 DE
 XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 XX
 OS Mus sp.
 DE
 XX WO9961629-A1.
 PN
 XX 02-DEC-1999.
 PD
 XX 24-MAY-1999; 99WO-JP02711.
 PF
 XX 25-MAY-1998; 98JP-0159957.
 PR
 XX 26-MAY-1998; 98JP-0163023.
 (ASAH) ASAH KASEI KOGYO KK.
 PA (ASAH) ASAH MEDICAL CO LTD.
 XX Ono M, Soka T, Morimoto I, Miyamura K;
 PI
 XX WPI: 2000-086720/07.
 DR N-PSDB; AA244232.
 DR
 XX Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells
 PT
 XX Disclosure; Page 97-98; 111pp; Japanese.
 PS
 CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD) positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 XX
 XX Sequence 111 AA;
 SQ
 Query Match 100.0%; Score 48; DB 21; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.64;
 Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQSSEDPPT 9
 Db 93 QQSSEDPPT 101
 |||||
 RESULT 8
 AAR32123
 ID AAR32123 standard; Protein; 131 AA.
 XX
 AC AAR32123;
 XX
 DT 02-JUN-1993 (first entry)
 DT
 XX Anti-CD4 antibody MT 3.10 light chain variable region.
 DE
 XX immunosuppression; tissue transplantation; graft; L chain; V region;
 KW T-helper cell inhibition; transplant rejection; MAb;
 KW interleukin-2 receptor.
 XX
 FH Key Location/Qualifiers

FT Peptide 1..20
 FT /label= signal
 FT Region 21..120
 FT /label= Variable
 FT Region 121..131
 FT /label= J1
 XX
 PN DE4143214-A.
 XX
 XX 28-JAN-1993.
 PD
 XX 30-DEC-1991; 91DE-4143214.
 PF
 XX 25-JUL-1991; 91DE-4124759.
 PR
 XX 30-DEC-1991; 91DE-4143214.
 (BOEF) BOEHRINGER MANNHEIM GMBH.
 PA
 XX Kaluza B, Riethmueller G, Scheuer W, Weidie U;
 PI
 XX WPI: 1993-037582/05.
 DR N-PSDB; AAQ36609.
 DR
 XX Synergistic antibody compsn. for use as immunosuppressant -
 PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
 PT alpha- or anti-IL2R beta antibodies
 PT
 XX Claim 5; Page 11; 18pp; German.
 PS
 XX This sequence is the light chain variable region of a preferred
 CC anti-CD4 monoclonal antibody for use in the claimed synergistic
 CC composition. MAB MT 3.10 is deposited as clone 3.101/SB10 (ECACC
 CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R
 CC alpha or beta antibody. Individually the antibodies are strongly
 CC inhibiting and when used together they immunosuppressive properties
 CC are improved; they synergistically inhibit T-helper cell
 CC proliferation to effectively inhibit transplant rejection at low
 CC doses without significantly reducing the general immune response.
 CC See also AAQ36608-Q36616.
 XX
 XX Sequence 131 AA;
 SQ
 Query Match 100.0%; Score 48; DB 14; Length 131;
 Best Local Similarity 100.0%; Pred. No. 0.76;
 Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQSSEDPPT 9
 Db 113 QQSSEDPPT 121
 |||||
 RESULT 9
 AAY59264
 ID AAY59264 standard; protein; 305 AA.
 XX
 AC AAY59264;
 XX
 DT 17-APR-2000 (first entry)
 DT
 XX Antibody 4H5 H chain sequence.
 DE
 XX CD4 antigen; anti-human; antibody; 4H5; drug.
 KW
 XX Mus sp.
 OS
 XX JPI1332563-A.
 PN
 XX 07-DEC-1999.
 PD
 XX 26-MAY-1998; 98JP-0163034.
 PF
 XX 26-MAY-1998; 98JP-0163034.
 PR
 XX

PA (ASAH) ASahi KASEI KOGYO KK.
 XX
 DR WPI; 2000-091351/08.
 DR N-PSDB; AA258663.

PT An antibody and the nucleic acid coding the antibody -

XX
 XX
 PS Disclosure; Page 16-17; 25pp; Japanese.

XX
 CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the H chain sequence of the antibody 4H5.

XX
 XX
 SQ Sequence 305 AA;

Query Match 100.0%; Score 48; DB 21; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9

DB 115 QOSSEDPPT 123

RESULT 10

AA59265
 ID AAY59265 standard; protein; 305 AA.

XX
 AC AAY59265;

XX
 DT 17-APR-2000 (first entry)

XX
 DE Antibody 4H5 L chain sequence.

XX
 KW CD4 antigen; anti-human; antibody; 4H5; drug.

XX
 OS Mus sp.

XX
 PN JP11332563-A.

XX
 PD 07-DEC-1999.

XX
 PF 26-MAY-1998; 98JP-0163034.

XX
 PR 26-MAY-1998; 98JP-0163034.

XX
 (ASAH) ASahi KASEI KOGYO KK.

XX
 WPI; 2000-091351/08.

XX
 DR N-PSDB; AA258664.

XX
 PT An antibody and the nucleic acid coding the antibody -

XX
 PS Disclosure; Page 17-18; 25pp; Japanese.

XX
 CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the L chain sequence of the antibody 4H5.

XX
 SQ Sequence 305 AA;

Query Match 100.0%; Score 48; DB 21; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9

DB 248 QOSSEDPPT 256

RESULT 11

AA51141
 ID AAY51141 standard; Protein; 305 AA.
 XX
 AC AAY51141;

XX
 DT 31-MAR-2000 (first entry)

XX
 DE Murine derived protein fragment #3.

XX
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.

XX
 OS Mus sp.

XX
 PN WO9961629-A1.

XX
 PD 02-DEC-1999.

XX
 PF 24-MAY-1999; 99WO-JP02711.

XX
 PR 25-MAY-1998; 98JP-0159957.

XX
 PR 26-MAY-1998; 98JP-0163023.

XX
 PA (ASAH) ASahi KASEI KOGYO KK.

XX
 PA (ASAH) ASahi MEDICAL CO LTD.

XX
 PI Ono M, Soka T, Morimoto I, Miyamura K;

XX
 WPI; 2000-086720/07.

XX
 DR N-PSDB; AA244205.

XX
 PT Devices containing antibodies recognising CD4 or CD34 and their use for
 the separation of CD4 or CD34 positive cells

XX
 PS Claim 22; Page 80-82; 11pp; Japanese.

XX
 CC This invention describes a novel device (I) for separating cluster
 differentiation (CD)-positive cells using a recombinant (chimeric or
 single-chain) antibody recognising CD4 or CD34. The devices are useful
 for the separation of CD4 or CD34 positive cells, which is useful for
 the collection of hematopoietic undifferentiated cells, elimination of
 lymphocytes from cells to be used in bone marrow transplantation, the
 detection of leukemic cells and the production of medicinal
 compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 to illustrate the method of the invention.

XX
 SQ Sequence 305 AA;

Query Match 100.0%; Score 48; DB 21; Length 305;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9

DB 115 QOSSEDPPT 123

RESULT 12

AA51142
 ID AAY51142 standard; Protein; 305 AA.

XX
 AC AAY51142;

XX
 DT 31-MAR-2000 (first entry)

XX
 DE Murine derived protein fragment #4.

XX
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.

OS Mus sp.
 XX WO9961629-A1.
 PN
 XX
 XX
 PD 02-DEC-1999.
 XX
 XX 24-MAY-1999; 99WO-JP02711.
 PF
 XX 25-MAY-1998; 98JP-0159957.
 PR
 XX 26-MAY-1998; 98JP-0163023.
 PR
 XX (ASAH) ASahi KASEI KOGYO KK.
 PA (ASAH) ASahi MEDICAL CO LTD.
 XX
 XX Ono M, Soka T, Morimoto I, Miyamura K;
 XX WPI; 2000-086720/07.
 DR N-PSDB; AAZ44206.
 XX
 XX Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells -
 PT
 PT Claim 22; Page 82-84; 111pp; Japanese.
 XX
 CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 XX
 XX Sequence 305 AA;
 SQ
 Query Match 100.0%; Score 48; DB 21; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQSSEDPPT 9
 Db 248 QQSSEDPPT 256
 |||:|||||
 RESULT 13
 AAR70197
 ID AAR70197 standard; Protein; 9 AA.
 XX
 XX AAR70197;
 DT 20-SEP-1995 (first entry)
 XX
 XX Mab 3B9 light chain CDR.
 DE
 XX Chimeric antibody; humanized antibody; antibody engineering;
 KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy; CDR;
 KW complementarity determining region.
 XX
 XX Mus sp.
 OS
 XX WO9507301-A.
 PN
 XX
 XX 16-MAR-1995.
 PD
 XX 07-SEP-1994; 94WO-US10308.
 PF
 XX 07-SEP-1993; 93US-0117366.
 PR
 XX 14-OCT-1993; 93US-0136783.
 PR
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX

Gross MS, Holmes SD, Sylvester DR;
 WPI; 1995-123387/16.
 Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 from high affinity mAbs - useful in treatment of IL-4-mediated
 and IgE-mediated allergic conditions
 Disclosure; Page 56; 97pp; English.
 Spleen cells from mice immunized with human IL-4 were used to prepare
 hybridomas, which were screened for anti-IL-4 Mab secretion. Only
 clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
 chains were cloned into pGEM7i+ and transformed into E. coli
 DH5-alpha. A light chain cDNA clone was sequenced (AAQ83490) that
 encoded the protein given in AAR70189. 3 CDRs (AAR70195-97) were
 identified.
 Query Match 93.8%; Score 45; DB 16; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.8e+05;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQSSEDPPT 9
 Db 1 QQSSEDPPT 9
 |||:|||||
 RESULT 14
 AAY23774
 ID AAY23774 standard; Peptide; 9 AA.
 XX
 XX AAY23774;
 DT 13-SEP-1999 (first entry)
 XX
 XX CDR of the light chain variable region of antibody 3B9.
 DE
 XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;
 KW allergy; complementarity determining region.
 XX
 XX Mus sp.
 OS
 XX US5928904-A.
 PN
 XX 27-JUL-1999.
 PD
 XX 07-JUN-1995; 95US-0483632.
 PF
 XX 07-JUN-1995; 95US-0483632.
 PR
 XX 07-SEP-1993; 93US-0117366.
 PR
 XX 14-OCT-1993; 93US-0136783.
 PR
 XX 07-SEP-1994; 94WO-US10308.
 PR
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Gross MS, Holmes SD, Sylvester DR;
 PI
 XX WPI; 1999-429500/36.
 DR N-PSDB; AAX85891.
 XX
 XX New DNA molecules encoding recombinant antibodies useful for
 PT treating IL4-mediated conditions
 XX
 XX Example 3; Column 45; 50pp; English.
 PS
 XX

CC The present sequence represents a complementarity determining region
 CC (CDR) of the light chain variable region of murine interleukin-4
 CC (IL-4) antibody 3B9. The specification describes chimeric and
 CC humanised IL-4 monoclonal antibodies. The antibodies of the
 CC invention are used in therapeutic and pharmaceutical compositions
 CC for treating IL-4 mediated and immunoglobulin E-mediated allergic
 CC reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis,
 CC atopic asthma, anaphylactic shock, rheumatoid arthritis,
 CC host-versus-graft disease and renal disease. They are also useful
 CC in the diagnosis of an allergy or condition associated with excess
 CC IL-4 production through the measurement e.g. by ELISA of circulating
 CC endogenous IL-4 levels in humans.
 XX
 XX

SQ Sequence 9 AA;

Query Match 93.8%; Score 45; DB 20; Length 9;

Best Local Similarity 88.9%; Pred. No. 7.8e+05;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 QQSSEDPPT 9

1 QQSSEDPPT 9

1 QQSSEDPPT 9

1 QQSSEDPPT 9

1 QQSSEDPPT 9

1 QQSSEDPPT 9

1 QQSSEDPPT 9

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1 QQSSEDPPT 9

1 QQSSEDPPT 9

1 QQSSEDPPT 9

1 QQSSEDPPT 9

1 QQSSEDPPT 9

1 QQSSEDPPT 9

CC versus host disease.

XX Sequence 9 AA;

SQ Sequence 9 AA;

Query Match 93.8%; Score 45; DB 20; Length 9;

Best Local Similarity 88.9%; Pred. No. 7.8e+05;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 QQSSEDPPT 9

1 QQSSEDPPT 9

1 QQSSEDPPT 9

1 QQSSEDPPT 9

1 QQSSEDPPT 9

1 QQSSEDPPT 9

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1 QQSSEDPPT 9

1 QQSSEDPPT 9

1 QQSSEDPPT 9

Search completed: February 14, 2003, 11:15:45

Job time : 24.3871 secs

CC This sequence represents a light chain complementarity determining region
 CC (CDR) from an antibody of the invention. The antibody is a chimeric or
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
 CC immunoglobulin E (IgE) mediated diseases. The antibodies are useful for
 CC the treatment of allergic disorders such as allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
 CC The antibodies are also useful for regulating B and T cell proliferation
 CC and as such are useful in the treatment of autoimmune diseases and graft



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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:13:07 : Search time 8.12903 Seconds
(without alignments)
32.575 Million cell updates/sec

Title: US-09-701-001b-6

Perfect score: 48

Sequence: 1 QOSSEDPPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	93.8	9	2	US-08-483-636-20
2	45	93.8	9	2	US-08-483-632-20
3	45	93.8	111	2	US-08-483-636-73
4	45	93.8	111	2	US-08-483-632-73
5	45	93.8	131	1	US-08-437-117D-33
6	45	93.8	131	2	US-08-436-717-33
7	45	93.8	131	2	US-08-621-751A-10
8	45	93.8	131	2	US-08-621-751A-14
9	45	93.8	131	2	US-08-483-636-58
10	45	93.8	131	2	US-08-483-632-58
11	45	93.8	132	2	US-08-483-636-2
12	45	93.8	132	2	US-08-483-632-2
13	40	83.3	9	2	US-08-483-636-28
14	40	83.3	9	2	US-08-483-632-28
15	40	83.3	131	2	US-08-483-636-14
16	40	83.3	131	2	US-08-483-632-14
17	37	77.1	9	4	US-09-170-769A-21
18	37	77.1	215	4	US-09-170-769A-4
19	36	75.0	15	2	US-08-945-168B-117
20	36	75.0	412	2	US-08-463-081B-14
21	36	75.0	412	2	US-08-461-379A-14
22	36	75.0	412	2	US-08-462-390B-14
23	36	75.0	412	3	US-08-463-074B-14
24	36	75.0	412	3	US-08-465-585C-14
25	36	75.0	412	3	US-08-652-446-14
26	36	75.0	412	4	US-09-462-624-2
27	35	72.9	9	5	PCT-US94-14106-42

28	34	70.8	9	5	PCT-US94-14106-43	Sequence 43, Appl
29	34	70.8	106	3	US-08-466-151-6	Sequence 6, Appli
30	34	70.8	106	4	US-08-466-163B-6	Sequence 8, Appli
31	34	70.8	111	1	US-08-491-845-8	Sequence 16, Appl
32	34	70.8	111	3	US-08-513-968-51	Sequence 51, Appl
33	34	70.8	115	3	US-08-579-378A-14	Sequence 14, Appl
34	34	70.8	131	4	US-08-579-378A-18	Sequence 18, Appl
35	34	70.8	131	4	US-08-579-378A-18	Sequence 2, Appli
36	34	70.8	218	5	PCT-US96-13152-2	Sequence 7, Appli
37	33	68.8	28	3	US-08-984-277-7	Sequence 5, Appli
38	33	68.8	111	2	US-08-887-352B-5	Sequence 6, Appli
39	33	68.8	111	3	US-08-887-352B-6	Sequence 2, Appli
40	33	68.8	111	3	US-08-466-151-2	Sequence 5, Appli
41	33	68.8	111	4	US-09-109-207C-5	Sequence 6, Appli
42	33	68.8	111	4	US-09-109-207C-6	Sequence 6, Appli
43	33	68.8	111	4	US-09-296-005-5	Sequence 6, Appli
44	33	68.8	111	4	US-09-296-005-6	Sequence 2, Appli
45	33	68.8	111	4	US-08-466-163B-2	

ALIGNMENTS

RESULT 1
US-08-483-636-20
; Sequence 20, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESS: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-483-636-20

Query Match 93.8%; Score 45; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
|:|:|:|:|:|:
Db 1 QOSNEDPPT 9

RESULT 2

US-08-483-632-20
; Sequence 20, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TREATMENT OF IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-632-20

Query Match 93.8%; Score 45; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
|:|:|:|:|:|:
Db 1 QOSNEDPPT 9

RESULT 3

US-08-483-636-73

; Sequence 73, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TREATMENT OF IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-483-636-73

Query Match 93.8%; Score 45; DB 2; Length 111;
Best Local Similarity 88.9%; Pred. No. 0.51;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
|:|:|:|:|:|:
Db 93 QOSNEDPPT 101

RESULT 4

US-08-483-632-73
; Sequence 73, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TREATMENT OF IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Smithkline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-483-632-73

Query Match 93.8%; Score 45; DB 2; Length 111;
Best Local Similarity 88.9%; Pred. No. 0.51;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
111:111111
93 QQSNEPDPT 101

RESULT 5
US-08-137-117D-33
Sequence 33, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-33

Query Match 93.8%; Score 45; DB 1; Length 131;
Best Local Similarity 88.9%; Pred. No. 0.6;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
111:111111
Db 113 QQSNEPDPT 121

RESULT 6
US-08-436-717-33
Sequence 33, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544

; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; 8-436-717-33

Query Match 93.8%; Score 45; DB 2; Length 131;
Best Local Similarity 88.9%; Pred. NO. 0.6;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
Db 113 QOSNEDPPT 121

RESULT 7
US-08-621-751A-10
; Sequence 10, Application US/08621751A
; Patent No. 5882644
; GENERAL INFORMATION:
; APPLICANT: Chang, Chung N.
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Martin, Ulrich
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER LLP
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,751A
; FILING DATE: 22-MAR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 321152000100
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141 MRSN FOERS SFO
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-621-751A-10

Query Match 93.8%; Score 45; DB 2; Length 131;
Best Local Similarity 88.9%; Pred. NO. 0.6;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
Db 113 QOSNEDPPT 121

RESULT 8
US-08-621-751A-14
; Sequence 14, Application US/08621751A
; Patent No. 5882644
; GENERAL INFORMATION:
; APPLICANT: Chang, Chung N.
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Martin, Ulrich
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER LLP
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,751A
; FILING DATE: 22-MAR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 321152000100
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141 MRSN FOERS SFO
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-621-751A-14

Query Match 93.8%; Score 45; DB 2; Length 131;
Best Local Similarity 88.9%; Pred. NO. 0.6;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
Db 113 QOSNEDPPT 121

RESULT 9
US-08-483-636-58
; Sequence 58, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.

TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-636-58

Query Match 93.8%; Score 45; DB 2; Length 131;
; Best Local Similarity 88.9%; Pred. No. 0.6;
; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; 1 QQSEDPPT 9
; |||:|||||
; Db 112 QQSNEPPT 120

RESULT 10
; US-08-483-632-58
; Sequence 58, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-632-58

Query Match 93.8%; Score 45; DB 2; Length 131;
; Best Local Similarity 88.9%; Pred. No. 0.6;
; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; 1 QQSEDPPT 9
; |||:|||||
; Db 112 QQSNEPPT 120

RESULT 11
; US-08-483-636-2
; Sequence 2, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIORITY INFORMATION:
PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-636-2

Query Match 93.8%; Score 45; DB 2; Length 132;
Best Local Similarity 88.9%; Pred. No. 0.6;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSSEDPT 9
Db 113 QQSNEPPT 121

RESULT 12
US-08-483-632-2
Sequence 2, Application US/08483632
Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TREATMENT OF IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-632-2

Query Match 93.8%; Score 45; DB 2; Length 132;
Best Local Similarity 88.9%; Pred. No. 0.6;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSSEDPT 9
Db 113 QQSNEPPT 121

RESULT 13
US-08-483-636-28
Sequence 28, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TREATMENT OF IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-636-28

Query Match 83.3%; Score 40; DB 2; Length 9;
Best Local Similarity 87.5%; Pred. No. 2e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDP 8
|11:1111
Db 1 QOSNEDPP 8

RESULT 14

US-08-483-632-28
; Sequence 28, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA: PCT/US/94/10308
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-632-28

Query Match 83.3%; Score 40; DB 2; Length 9;
Best Local Similarity 87.5%; Pred. No. 2e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDP 8
|11:1111
Db 1 QOSNEDPP 8

RESULT 15

US-08-483-636-14
; Sequence 14, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.

; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA: PCT/US/94/10308
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-636-14

Query Match 83.3%; Score 40; DB 2; Length 131;
Best Local Similarity 87.5%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDP 8
|11:1111
Db 112 QOSNEDPP 119

Search completed: February 14, 2003, 11:20:50
Job time: 8.12903 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:15:53 ; Search time 5.22581 Seconds
(without alignments)
44.001 Million cell updates/sec

Title: US-09-701-001B-6
Perfect score: 48
Sequence: 1 QOSSEDPPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	45	93.8	9	US-09-879-461-20	Sequence 20, Appl
2	45	93.8	112	US-09-144-886-80	Sequence 80, Appl
3	45	93.8	131	US-09-879-461-58	Sequence 58, Appl
4	45	93.8	132	US-09-879-461-2	Sequence 2, Appl
5	40	83.3	9	US-09-879-461-28	Sequence 28, Appl
6	40	83.3	131	US-09-879-461-14	Sequence 14, Appl
7	36	75.0	134	US-09-881-823-2	Sequence 2, Appl
8	36	75.0	412	US-10-078-650-17	Sequence 17, Appl
9	36	75.0	412	US-10-094-649-2	Sequence 2, Appl
10	35	72.9	112	US-09-144-886-81	Sequence 81, Appl
11	35	72.9	112	US-09-810-502-36	Sequence 36, Appl
12	35	72.9	112	US-09-810-502-37	Sequence 37, Appl
13	35	72.9	780	US-09-771-161A-144	Sequence 144, App
14	35	72.9	942	US-09-771-161A-235	Sequence 235, App
15	35	72.9	942	US-09-771-161A-236	Sequence 236, App
16	34	70.8	106	US-09-802-077-6	Sequence 6, Appl
17	34	70.8	106	US-09-802-096-6	Sequence 6, Appl
18	34	70.8	112	US-09-144-886-87	Sequence 87, Appl
19	34	70.8	218	US-09-917-410-2	Sequence 2, Appl

20	33	68.8	61	9	US-09-796-692-1514	Sequence 1514, Ap
21	33	68.8	97	9	US-10-001-883-91	Sequence 91, Appl
22	33	68.8	111	10	US-09-802-077-2	Sequence 2, Appl
23	33	68.8	111	10	US-09-802-096-2	Sequence 2, Appl
24	33	68.8	111	10	US-09-920-171-5	Sequence 5, Appl
25	33	68.8	111	10	US-09-920-171-6	Sequence 6, Appl
26	33	68.8	114	10	US-09-920-171-8	Sequence 8, Appl
27	33	68.8	114	10	US-09-920-171-9	Sequence 9, Appl
28	33	68.8	114	10	US-09-920-171-10	Sequence 10, Appl
29	33	68.8	175	10	US-09-925-122A-3	Sequence 3, Appl
30	33	68.8	218	10	US-09-802-077-9	Sequence 9, Appl
31	33	68.8	218	10	US-09-802-096-9	Sequence 9, Appl
32	33	68.8	218	10	US-09-920-171-13	Sequence 13, Appl
33	33	68.8	218	10	US-09-920-171-15	Sequence 15, Appl
34	33	68.8	218	10	US-09-920-171-17	Sequence 17, Appl
35	33	68.8	218	10	US-09-920-171-19	Sequence 19, Appl
36	33	68.8	218	10	US-09-920-171-24	Sequence 24, Appl
37	33	68.8	248	10	US-09-920-171-22	Sequence 22, Appl
38	33	68.8	248	10	US-09-920-171-23	Sequence 23, Appl
39	33	68.8	348	9	US-09-738-626-4325	Sequence 4325, Ap
40	32	66.7	359	9	US-09-712-363-269	Sequence 269, App
41	32	66.7	92	10	US-09-893-737-204	Sequence 204, Appl
42	32	66.7	112	9	US-09-144-886-84	Sequence 84, Appl
43	32	66.7	112	9	US-09-144-886-85	Sequence 85, Appl
44	32	66.7	112	9	US-09-144-886-86	Sequence 86, Appl
45	32	66.7	112	9	US-09-144-886-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1
US-09-879-461-20
; Sequence 20, Application US/09879461
; Publication No. US20020193575A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; Gross, Mitchell S.
; Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property, UW2220 - 709
; Swedeland Rd.
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-879-461-20

Query Match          93.8%; Score 45; DB 9; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
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Db 1 QOSNEPDPT 9

RESULT 2
US-09-144-886-80
; Sequence 80, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bont/A clone
; OTHER INFORMATION: IB6 region VL epitope 1
US-09-144-886-80

Query Match          93.8%; Score 45; DB 9; Length 112;
Best Local Similarity 88.9%; Pred. No. 0.28;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
   |||:|||||
Db 93 QOSNEPDPT 101

RESULT 3
US-09-879-461-58
; Sequence 58, Application US/09879461
; Publication No. US20020193575A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property, UW2220 - 709
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
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;
; APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-879-461-58

Query Match          93.8%; Score 45; DB 9; Length 131;
Best Local Similarity 88.9%; Pred. No. 0.33;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
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Db 112 QOSNEPDPT 120

RESULT 4
US-09-879-461-2
; Sequence 2, Application US/09879461
; Publication No. US20020193575A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property, UW2220 - 709
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-879-461-2

Query Match 93.8%; Score 45; DB 9; Length 132;
Best Local Similarity 88.9%; Pred. No. 0.33;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9
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DB 113 QQSNEPPT 121

LT 5
US-879-461-28
Sequence 28, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Sylvester, Daniel R.

TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders

NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA

COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-09-879-461-28
Query Match 83.3%; Score 40; DB 9; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.2e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 8
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DB 1 QQSNEPPT 8

RESULT 6

US-09-879-461-14
Sequence 14, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:

APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders

NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.

CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-879-461-14

Query Match 83.3%; Score 40; DB 9; Length 131;
Best Local Similarity 87.5%; Pred. No. 2.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 8
| | | : | | | | |

DB 112 QQSNEPPT 119

RESULT 7

US-09-881-823-2
Sequence 2, Application US/09881823
Patent No. US20020068066A1
GENERAL INFORMATION:

APPLICANT: SHI, WENYUAN
ANDERSON, MAXWELL
MORRISON, SHERIE
TRINH, RYAN
WIMS, LETITIA
CHEN, LI

TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries

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; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881.823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Murine
US-09-881-823-2
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Query Match 75.0%; Score 36; DB 10; Length 134;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 QOSSEDPPT 9
Db 113 QONNADPPT 121
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US-10-078-650-17
; Sequence 17, Application US/10078650
; Patent No. US20020169301A1
; GENERAL INFORMATION:
; APPLICANT: Fujimoto, Katsumi
; APPLICANT: Shin, Mei
; APPLICANT: Kato, Yukio
; TITLE OF INVENTION: NOVEL bHLH TYPE TRANSCRIPTION FACTOR
; FILE REFERENCE: 06501-101001
; CURRENT APPLICATION NUMBER: US/10/078,650
; PRIOR FILING DATE: 2002-02-19
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: JP 11-233286
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-078-650-17
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Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 QOSSEDPPT 9
Db 279 KOESEEPPT 287
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US-10-094-649-2
; Sequence 2, Application US/10094649
; Publication No. US20030009020A1
; GENERAL INFORMATION:
; APPLICANT: Kawamoto, Takeshi
; APPLICANT: Kato, Yukio
; TITLE OF INVENTION: Gene Originating in Human Chondrocyte
; FILE REFERENCE: 46124-5014-US
; CURRENT APPLICATION NUMBER: US/10/094,649
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US/09/462,624
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 202227/1997
; PRIOR FILING DATE: 1997-07-11
; PRIOR APPLICATION NUMBER: PCT/JP98/03106
; PRIOR FILING DATE: 1998-07-10
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; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-649-2
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Query Match 75.0%; Score 36; DB 9; Length 412;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 QOSSEDPPT 9
Db 279 KOESEEPPT 287
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US-09-144-886-81
; Sequence 81, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500-117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
US-09-144-886-81
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Query Match 72.9%; Score 35; DB 9; Length 112;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 QOSSEDPPT 9
Db 93 QOSNEDPPT 101
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US-09-810-502-36
; Sequence 36, Application US/09810502
; Patent No. US20020034765A1
; GENERAL INFORMATION:
; APPLICANT: Padlan, Eduardo A.
; Daugherty, Bruce L.
; Mark, George E.
; TITLE OF INVENTION: A METHOD FOR REDUCING THE IMMUNOGENICITY
; OF ANTIBODY VARIABLE DOMAINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/810,502
; FILING DATE: 16-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/905,280
; FILING DATE: 01-Aug-1997
; APPLICATION NUMBER: 08/609,218
; FILING DATE: 01-Mar-1996
; APPLICATION NUMBER: 08/109,187
; FILING DATE: 19-Aug-1993
; APPLICATION NUMBER: 07/702,217
; FILING DATE: 17-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18410CC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3905
; TELEFAX: 732-594-4720
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-810-502-36

Query Match 72.9%; Score 35; DB 10; Length 112;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9
| | | | | | |
Db 93 QQSNEPPLT 101

RESULT 12

US-09-810-502-37
; Sequence 37, Application US/09810502
; Patent No. US20020034765A1
; GENERAL INFORMATION:
; APPLICANT: Padlan, Eduardo A.
; Daugherty, Bruce L.
; Mark, George E.

TITLE OF INVENTION: A METHOD FOR REDUCING THE IMMUNOGENICITY
OF ANTIBODY VARIABLE DOMAINS

NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0907

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/810,502
FILING DATE: 16-Mar-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/905,280
FILING DATE: 01-Aug-1997
APPLICATION NUMBER: 08/609,218
FILING DATE: 01-Mar-1996
APPLICATION NUMBER: 08/109,187
FILING DATE: 19-Aug-1993

; APPLICATION NUMBER: 07/702,217
; FILING DATE: 17-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18410CC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3905
; TELEFAX: 732-594-4720
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-810-502-37

Query Match 72.9%; Score 35; DB 10; Length 112;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9
| | | | | | |
Db 93 QQSNEPPLT 101

RESULT 13

US-09-771-161A-144
; Sequence 144, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.

TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771.161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 144
LENGTH: 780
TYPE: PRT
ORGANISM: Homo sapiens

US-09-771-161A-144

Query Match 72.9%; Score 35; DB 10; Length 780;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9
| | | | | | |
Db 564 QKSRRDPPS 572

RESULT 14

US-09-771-161A-235
; Sequence 235, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.

TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771.161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676

; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 235
; LENGTH: 942
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-235

Query Match 72.9%; Score 35; DB 10; Length 942;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
Db 564 QKSRDPPS 572

US-09-771-161A-236
; Sequence 236, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 236
; LENGTH: 942
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-236

Query Match 72.9%; Score 35; DB 10; Length 942;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
Db 564 QKSRDPPS 572

Search completed: February 14, 2003, 11:21:32
Job time : 6.22581 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:12:02 ; Search time 9 Seconds
(without alignments)
96.134 Million cell updates/sec

Title: US-09-701-001b-6
Perfect score: 48
Sequence: 1 QOSSEDPPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73: *
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	112	2 S19971	Ig kappa chain V r
2	48	100.0	131	2 PH1226	Ig kappa chain pre
3	38	79.2	112	2 S19972	Ig kappa chain V r
4	38	79.2	301	2 T45859	R2R3-MYB transcrip
5	38	79.2	304	1 S71285	myb-related protei
6	37	77.1	508	2 F84921	hypothetical prote
7	36	75.0	65	2 C38601	Ig kappa chain V r
8	36	75.0	412	2 JC5547	basic helix-loop-h
9	35	72.9	96	2 B49442	Ig light chain V r
10	35	72.9	102	2 PH1079	Ig light chain V r
11	35	72.9	107	2 S26344	Ig kappa chain V r
12	35	72.9	111	1 KVMS37	Ig kappa chain V r
13	35	72.9	111	1 KVMS31	Ig kappa chain V r
14	35	72.9	111	1 KVMS83	Ig kappa chain V r
15	35	72.9	111	1 S09966	Ig kappa chain V-J
16	35	72.9	111	2 A33936	Ig kappa chain V r
17	35	72.9	479	2 S48705	serine/threonine p
18	35	72.9	942	2 JC2129	protein kinase PKN
19	35	72.9	950	2 S27473	URB51 protein - sm
20	34	70.8	107	2 S26343	Ig kappa chain V r
21	34	70.8	111	1 KVMS43	Ig kappa chain V r
22	34	70.8	111	1 KVMS08	Ig kappa chain V r
23	34	70.8	111	1 KVMS69	Ig kappa chain V r
24	34	70.8	127	2 B4172	hypothetical prote
25	34	70.8	268	2 T51678	myb-related transc
26	34	70.8	320	2 C85440	myb-related protei
27	34	70.8	355	2 AE0034	probable type III
28	34	70.8	794	2 T27870	hypothetical prote
29	34	70.8	925	2 JC2033	G protein-coupled

30	34	70.8	1006	2 T00050	hypothetical prote
31	34	70.8	1027	2 I38604	p53-binding protei
32	34	70.8	3149	1 BQBE8	BPLF1 protein - hu
33	33	68.8	62	1 NINJ1M	short neurotoxin 1
34	33	68.8	81	2 S42193	Ig kappa chain V r
35	33	68.8	87	2 C97796	hypothetical prote
36	33	68.8	111	2 D45722	anti-glycoprotein
37	33	68.8	135	2 D82539	hypothetical prote
38	33	68.8	192	2 T35200	hypothetical prote
39	33	68.8	359	2 A70978	probable rmlA2 pro
40	33	68.8	491	2 JE0276	voltage-gated pota
41	33	68.8	731	2 S46813	lanosterol synthas
42	33	68.8	786	2 A5501	cyclin F - human
43	33	68.8	1094	2 S49313	protein kinase - s
44	33	68.8	1392	2 A43336	microtubule-vesicl
45	33	68.8	1427	2 S22695	restin - human

ALIGNMENTS

RESULT 1

S19971

Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
R:Accession: S19971; S19973
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19971
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65091; NID:g52288; PIDN:CAA46219.1; PID:g52289
A:Experimental source: clone M-T310
A:Accession: S19973
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PID:g52293
A:Experimental source: M-T404
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
Db 93 QOSSEDPPT 101

RESULT 2

PH1226

Ig kappa chain precursor V region (M-T310) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
R:Accession: PH1226
R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; L
Gene 121, 271-278, 1992
A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and
A:Reference number: PH1224; MUID:93077041; PMID:1446824
A:Accession: PH1226
A:Molecule type: mRNA
A:Residues: 1-131 <WEI>
A:Cross-references: GB:S50265; NID:g260765; PIDN:AA24320.1; PID:g260766
A:Note: this mouse sequence was hybridized and fused with a human constant region gen
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-131/Product: Ig light chain V region #status predicted <MAT>

F;36-114/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSSEDPPT 9
| | | | | | | | | |
Db 113 QOSSEDPPT 121

RESULT 3

S19972 Ig kappa chain V region (M-T321) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19972
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19972
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65094; NID:g52290; PIDN:CAA46222.1; PID:g52291
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 38; DB 2; Length 112;
Best Local Similarity 88.9%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSSEDPPT 9
| | | | | | | | | |
Db 93 QOSSEDPPT 101

RESULT 4

T45859 R2R3-MYB transcription factor - Arabidopsis thaliana

N:Alternate names: protein F3A4.140
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Mar-2000
C:Accession: T45859
R:Barques, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23007
A:Accession: T45859
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <BAR>
A:Cross-references: EMBL:AL132978
A:Experimental source: cultivar Columbia; BAC clone F3A4
C:Genetics:
A:Map position: 3
A:Note: F3A4.140
C:Superfamily: Arabidopsis myb-related 33.2K protein; myb DNA-binding repeat homology

Query Match 79.2%; Score 38; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SSEDPT 9
| | | | | | | | | |
Db 197 SSEDPT 203

RESULT 5

S71285 myb-related protein, 33.2K - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 16-Jun-2000
C:Accession: S71285
R:Kirik, V.; Baumllein, H.
submitted to the EMBL Data Library, September 1995
A:Description: Characterization of two cDNAs encoding MYB-related proteins in Arabid
A:Reference number: S71285
A:Accession: S71285
A:Molecule type: mRNA
A:Residues: 1-304 <KIR>
A:Cross-references: EMBL:Z54137; NID:g1263096; PIDN:CAA90810.1; PID:g1263097
C:Superfamily: Arabidopsis myb-related 33.2K protein; myb DNA-binding repeat homology
C:Keywords: DNA binding; duplication
F;1-52/Domain: myb DNA-binding repeat homology <MYB1>
F;53-103/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 79.2%; Score 38; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SSEDPT 9
| | | | | | | | | |
Db 197 SSEDPT 203

RESULT 6

F84921

hypothetical protein At2g47960 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: F84921
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, J.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84921
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-508 <STO>
A:Cross-references: GB:AE002093; NID:g3738308; PIDN:AAC63650.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g47960
A:Map position: 2

Query Match 77.1%; Score 37; DB 2; Length 508;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSSEDPPT 9
| | | | | | | | | |
Db 241 EDSTEDPT 249

RESULT 7

C38601

Ig kappa chain V region (2B5) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: C38601
R:Goshorn, S.C.; Retzel, E.; Jemerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same anti
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: C38601
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-65 <GOS>
A:Cross-references: GB:M57980; NID:g196406; PIDN:AAA63361.1; PID:g196407
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 75.0%; Score 36; DB 2; Length 65;

Best Local Similarity 77.8%; Pred. No. 5.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9
|||:||||
Db 46 QQSNEPPT 54

RESULT 8

JC5547
basic helix-loop-helix factor DEC1 - human
C:Species: Homo sapiens (man)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 21-Jul-2000
C:Accession: JC5547
R;Shen, M.; Kawamoto, T.; Yan, W.; Nakamasu, K.; Tamagami, M.; Koyano, Y.; Noshiro, M.;
Biochem. Biophys. Res. Commun. 236, 294-298, 1997
A:Title: Molecular characterization of the novel basic helix-loop-helix protein DEC1 ex
Reference number: JC5547; MUID:97382424; PMID:9240428
Accession: JC5547
Molecule type: mRNA
A:Residues: 1-412 <SHE>
A:Cross-references: DDBJ:AB004066; NID:q2308996; PIDN:BAA21720.1; PID:q2308997
C:Comment: This protein is involved in the control of cell differentiation in several ti
F;51-108/Region: helix-loop-helix #status predicted

Query Match 75.0%; Score 36; DB 2; Length 412;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9
:|||||
Db 279 QQSSEPT 287

RESULT 9

B49442
Ig light chain V region (50.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: B49442
R;Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.; S
Proteins 14, 499-508, 1992
A:Title: Crystallization, sequence, and preliminary crystallographic data for an antipe
A:Reference number: A49442; MUID:93066166; PMID:1438187
A:Accession: B49442
A:Status: preliminary; not compared with conceptual translation
Molecule type: DNA
A:Residues: 1-96 <STU>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F;8-86/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 35; DB 2; Length 96;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9
|||:||||
Db 85 QQSNEPPT 93

RESULT 10

PH1079
Ig light chain V region (clone 202.38m) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1079
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1079
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-102 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 35; DB 2; Length 102;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9
|||:||||
Db 93 QQSKEVPT 101

RESULT 11

S26344
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26344
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protei
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26344
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <STA>
A:Cross-references: EMBL:X59209; NID:q52336; PIDN:CAA41919.1; PID:g1334074
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-93/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 35; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9
|||:||||
Db 92 QQSNEPPT 100

RESULT 12

KVMS37
Ig kappa chain V regions (PC3741, T111) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 21-Jan-2000
C:Accession: A93204; A93822; A01934
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Contents: PC3741
A:Accession: A93204
A:Molecule type: protein
A:Residues: 1-111 <WEI>
R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related
A:Reference number: A93822; MUID:79012520; PMID:99744
A:Contents: T111
A:Accession: A93822
A:Molecule type: protein
A:Residues: 1-111 <MCK>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted

```
Query Match          72.9%; Score 35; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
DB 93 QOSNEDPYT 101

RESULT 13
KWMS83
Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000
C:Accession: A01936
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related molecules
A:Reference number: A93822; MUID:79012520; PMID:99744
A:Accession: A01936
A:Molecule type: protein
A:Residues: 1-111 <MCK>
Comment: This chain was isolated from a myeloma protein.
Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match          72.9%; Score 35; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
DB 93 QOSNEDPYT 101

RESULT 14
KWMS83
Ig kappa chain V region (PC7183) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: B01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Accession: B01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match          72.9%; Score 35; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
DB 93 QOSNEDPYT 101

RESULT 15
S09966
Ig kappa chain V-J region (1E10) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
```

```
C:Accession: S09966
R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibody
A:Reference number: S09955; MUID:90269328; PMID:2347362
A:Accession: S09966
A:Molecule type: mRNA
A:Residues: 1-111 <REI>
A:Cross-references: EMBL:X51854; NID:955397; PIDN:CAA36147.1; PID:9930231
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match          72.9%; Score 35; DB 2; Length 111;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
DB 93 QOSNEDPYT 101
```

Search completed: February 14, 2003, 11:19:48
Job time : 10 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:05:27 ; Search time 4.64516 Seconds
(without alignments)
80.360 Million cell updates/sec

Title: US-09-701-001B-6
Perfect score: 48
Sequence: 1 QSSSEDPPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	75.0	411	1 BHB2_MOUSE	O35185 mus musculus
2	36	75.0	411	1 BHB2_RAT	O35780 rattus norv
3	36	75.0	412	1 BHB2_HUMAN	O14503 homo sapien
4	35	72.9	111	1 KV3H_MOUSE	P01660 mus musculus
5	35	72.9	111	1 KV3L_MOUSE	P01664 mus musculus
6	35	72.9	111	1 KV3N_MOUSE	P01666 mus musculus
7	35	72.9	942	1 KRL1_HUMAN	O16512 homo sapien
8	35	72.9	950	1 UBL1_USTMA	P40349 ustilago ma
9	34	70.8	111	1 KV3M_MOUSE	P01665 mus musculus
10	34	70.8	111	1 KV3O_MOUSE	P01667 mus musculus
11	34	70.8	111	1 KV3Q_MOUSE	P01669 mus musculus
12	34	70.8	215	1 VIF_HV2NZ	P05901 human immun
13	34	70.8	232	1 SPIH_HUMAN	O99865 homo sapien
14	34	70.8	925	1 GLHR_ANTEL	P35409 anthopleura
15	34	70.8	1972	1 P53L_HUMAN	Q28888 homo sapien
16	34	70.8	3149	1 TEGU_EBV	P01431 naja mossam
17	33	68.8	62	1 NXSL_NAJMO	O70624 human immun
18	33	68.8	118	1 REV_HV1LW	O88396 mus musculus
19	33	68.8	224	1 GRE2_MOUSE	Q15642 homo sapien
20	33	68.8	545	1 CIP4_HUMAN	P38604 saccharomyc
21	33	68.8	730	1 ERG7_YEAST	P41002 homo sapien
22	33	68.8	786	1 CG2F_HUMAN	O88879 mus musculus
23	33	68.8	1249	1 APAF_MOUSE	O99ev5 rattus norv
24	33	68.8	1249	1 APAF_RAT	P30622 homo sapien
25	33	68.8	1427	1 REST_HUMAN	P01662 mus musculus
26	32	66.7	111	1 KV3J_MOUSE	P01663 mus musculus
27	32	66.7	111	1 KV3K_MOUSE	P09711 human cytom
28	32	66.7	277	1 J1L1_HCMVA	O93379 ictalurus p
29	32	66.7	376	1 P53_ICTPU	P97497 mus musculus
30	32	66.7	403	1 SHBG_MOUSE	P54998 rhodococcus
31	32	66.7	417	1 SOXC_RHOSO	Q01988 canis famil
32	32	66.7	445	1 UBPE_CANFA	O00515 homo sapien
33	32	66.7	517	1 LAD1_HUMAN	

RESULT 1

ID	BHB2_MOUSE	STANDARD;	PRT;	411 AA.
AC	O35185; P97289;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DE	Class B basic helix-loop-helix protein 2 (BHLHB2) (Stimulated with retinoic acid 13) (E47 interaction protein 1) (eip1).			
GN	BHLHB2 OR STRA13 OR CLAST5.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
ON	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Embryonic carcinoma;			
RX	MEDLINE=97427857; PubMed=9284045;			
RA	Boudjelal M., Taneja R., Matsubara S., Bouillet P., Dolle P., Chambon P.;			
RT	"Overexpression of Stral3, a novel retinoic acid-inducible gene of the basic helix-loop-helix family, inhibits mesodermal and promotes neuronal differentiation of Pl9 cells.";			
RT	Genes Dev. 11:2052-2065(1997).			
RL	[2]			
RN	SEQUENCE FROM N.A., AND INTERACTION WITH E47/TCF3.			
RC	STRAIN=BALB/C;			
RX	MEDLINE=97203270; PubMed=9050988;			
RA	Dear T.N., Hainzl T., Follo M., Wilmore H., Matena K., Boehm T.;			
RT	"Identification of interaction partners for the basic-helix-loop-helix protein E47.";			
RT	OncoGene 14:891-898(1997).			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6; TISSUE=Spleen;			
RA	O-Wang J.;			
RT	"Isolation of a CD40-activated gene from murine splenic B cells.";			
RT	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Straussberg R.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: May function as a transcriptional factor for neuronal differentiation.			
CC	-!- SUBUNIT: Able to homodimerize or heterodimerize with E47.			
CC	-!- SUBCELLULAR LOCATION: Nuclear (By similarity).			
CC	-!- DEVELOPMENTAL STAGE: Expressed from E9.5 day to E17.5 day in the ventricular layer of the brain and spinal cord, but also in the retinal pigment epithelium, developing eyelids, nasal epithelium, serous gland, vibrissae, epithelium of the mouth cavity and the tooth buds. Highly expressed in the heart, thymus and adrenal glands followed by lung, liver parenchyma, kidney tubules, epithelium of the esophagus and stomach. From E15.5 to E17.5 it is expressed in urinary bladder and urethra. From E17.5, it is			

O9umx9 homo sapien
P45897 caenorhabdi
P20794 mus musculu
Q61545 mus musculu
Q01844 homo sapien
P24482 saccharomyc
Q60446 cricetus
Q92598 homo sapien
Q61699 mus musculu
P52593 saccharomyc
P07293 oryctolagus
P05830 escherichia

expressed in developing muscle.
 CC -!- INDUCTION: Stimulated by retinoic acid (RA).
 CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS.
 CC -!- SIMILARITY: CONTAINS 1 ORANGE DOMAIN.
 CC
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 CC
 CC EMBL: AF010305; AAB64228.1; -
 CC EMBL: Y07836; CA69169.1; -
 CC EMBL: AF364051; AAK50859.1; -
 CC EMBL: BC010720; AAH10720.1; -
 CC MGD: MGI:1097714; Bhlhb2.
 CC InterPro: IPR001092; HLH_basic.
 CC InterPro: IPR003650; Orange.
 CC Pfam: PF00010; HLH; 1.
 CC SMART: SM00353; HLH; 1.
 CC SMART: SM00511; ORANGE; 1.
 CC PROSITE: PS00038; HLH_1; 1.
 CC PROSITE: PS50888; HLH_2; 1.
 CC Transcription regulation; DNA-binding; Nuclear protein.
 CC DNA_BIND 53 65 BASIC DOMAIN.
 CC DOMAIN 66 108 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 CC DOMAIN 140 184 ORANGE.
 CC CONFLICT 288 288 K -> T (IN REF. 2).
 CC SEQUENCE 411 AA; 45360 MW; B392893CD49292BC CRC64;

Query Match 75.0%; Score 36; DB 1; Length 411;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSSEDPPT 9
 Db 279 KOSEEPPT 287

RESULT 2
 BHB2_RAT
 ID BHB2_RAT STANDARD; PRT; 411 AA.
 AC O35780.
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Class B basic helix-loop-helix protein 2 (bHLHB2) (Enhancer-of-split
 DE and hairy-related protein 2) (SHARP-2).
 GN BHLHB2 OR SHARP2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Hippocampus;
 RX MEDLINE=98193761; PubMed=9532582;
 RA Rossner M.J., Doer J., Gass P., Schwab M.H., Nave K.-A.;
 RT "SHARPs: mammalian enhancer-of-split- and hairy-related proteins
 RT coupled to neuronal stimulation.";
 RL Mol. Cell. Neurosci. 10:460-475(1997).
 CC -!- FUNCTION: May function as a transcriptional factor for neuronal
 CC differentiation.
 CC -!- SUBUNIT: Able to homodimerize or heterodimerize with E47 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung,
 CC liver, muscle, kidney, uterus and gut.
 CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS.

CC -!- SIMILARITY: CONTAINS 1 ORANGE DOMAIN.

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CC EMBL: AF009330; AAB63587.1; -
 CC InterPro: IPR001092; HLH_basic.
 CC InterPro: IPR003650; Orange.
 CC Pfam: PF00010; HLH; 1.
 CC SMART: SM00353; HLH; 1.
 CC SMART: SM00511; ORANGE; 1.
 CC PROSITE: PS00038; HLH_1; 1.
 CC PROSITE: PS50888; HLH_2; 1.
 CC Transcription regulation; DNA-binding; Nuclear protein.
 CC DNA_BIND 53 65 BASIC DOMAIN.
 CC DOMAIN 66 108 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 CC DOMAIN 140 184 ORANGE.
 CC SEQUENCE 411 AA; 45529 MW; E56BD468D08824AD CRC64;

Query Match 75.0%; Score 36; DB 1; Length 411;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSSEDPPT 9
 Db 279 KOSEEPPT 287

RESULT 3
 BHB2_HUMAN
 ID BHB2_HUMAN STANDARD; PRT; 412 AA.
 AC O14503; Q96TD3;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Class B basic helix-loop-helix protein 2 (bHLHB2) (Differentially
 DE expressed in chondrocytes protein 1) (DEC1) (Enhancer-of-split and
 DE hairy-related protein 2) (SHARP-2) (Stimulated with retinoic acid 13).
 GN BHLHB2 OR DEC1 OR SHARP2 OR STRA13.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Cartilage;
 RX MEDLINE=97382424; PubMed=9240428;
 RA Shen M., Kawamoto T., Yan W., Nakamasu K., Tamagami M., Koyano Y.,
 RA Noshiro M., Kato Y.;
 RT "Molecular characterization of the novel basic helix-loop-helix
 RT protein DEC1 expressed in differentiated human embryo chondrocytes.";
 RL Biochem. Biophys. Res. Commun. 236:294-298(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Leukocyte;
 RX MEDLINE=21125593; PubMed=11226878;
 RA Teramoto M., Nakamasu K., Noshiro M., Matsuda Y., Gotoh O., Shen M.,
 RA Tsutsumi S., Kawamoto T., Iwamoto Y., Kato Y.;
 RT "Gene structure and chromosomal location of a human bHLH
 RT transcriptional factor DEC1 x Stra13 x SHARP-2/bHLHB2.";
 RL J. Biochem. 129:391-396(2001).
 RN [3]
 RP SEQUENCE OF 4-412 FROM N.A.
 RC Ivanov S.V., Lerman M.I.;
 RA "Exon-intron structure of the human STRA13(DEC1) bHLH transcription
 RT factor gene.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]

```
RP UBIQUITINATION.
RX MEDLINE=21226780; PubMed=11278694;
RA Ivanova A.V., Ivanov S.V., Danilkovitch-Miagkova A., Lerman M.I.;
RT "Regulation of STRA13 by the von Hippel-Lindau tumor suppressor
RT protein, hypoxia, and the UBC9/ubiquitin proteasome degradation
RT pathway.";
RL J. Biol. Chem. 276:15306-15315(2001).
CC -!- FUNCTION: May function as a transcriptional factor to modulate
CC chondrogenesis in response to the CAMP pathway.
CC -!- SUBUNIT: Able to homodimerize or heterodimerize with E47.
CC Interacts with ubiquitin-conjugating enzyme (UBC9).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Expressed in cartilage, spleen, intestine,
CC lung, and to a lesser extent in heart, brain, liver, muscle and
CC stomach.
CC -!- PTM: Association with UBC9 may target the protein for proteolysis
CC by the ubiquitin-dependent proteasome pathway.
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSSCRIPTION FACTORS.
CC -!- SIMILARITY: CONTAINS 1 ORANGE DOMAIN.
CC -----
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CC -----
DR EMBL; AB004066; BAA21720.1; -
DR EMBL; AB043885; BAB18565.1; -
DR EMBL; AF353635; AAK49525.1; -
DR EMBL; AF353634; AAK49525.1; JOINED.
DR GenBank; HGNC:1046; BHLHB2.
DR MIM; 604256; -
DR InterPro; IPR001092; HLH_bas.
DR InterPro; IPR003650; Orange.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00511; ORANGE; 1.
DR PROSITE; PS00038; HLH_1; 1.
DR PROSITE; PS00888; HLH_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein;
KW Ub1 conjugation.
FT DNA_BIND 53 65 BASIC DOMAIN.
FT DOMAIN 66 108 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT DOMAIN 140 184 ORANGE.
FT SEQUENCE 412 AA; 45510 MW; 2D73A3D4980793E5 CRC64;
Query Match 75.0%; Score 36; DB 1; Length 412;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QOSSEDPPT 9
Db 279 QOSEEPPT 287
RESULT 4
KV3H_MOUSE
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
MEDLINE=79073152; PubMed=103003;
Qy 1 QOSSEDPPT 9
Db 279 QOSEEPPT 287
RESULT 4
KV3H_MOUSE
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
MEDLINE=79073152; PubMed=103003;
```

```
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -!- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR; A01934; KVM537.
DR HSSP; P01679; 2FB7.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
FT SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;
Query Match 72.9%; Score 35; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 4.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QOSSEDPPT 9
Db 93 QOSNEDPYT 101
RESULT 5
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVM5C1.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
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FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2BIAD98AD965962 CRC64;

Query Match 72.9%; Score 35; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 4.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
Db 93 QOSNEPDT 101

RESULT 6
KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase C-like 1 (EC 2.7.1.-) (Protein-kinase C-related kinase
DE 1) (Protein kinase C-like PKN) (Serine-threonine protein kinase N).
GN PRKCL1 OR PRK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

Query Match 72.9%; Score 35; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 4.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
Db 93 QOSNEPDT 101

RESULT 7
PKL1_HUMAN STANDARD; PRT; 942 AA.
AC Q16512; Q15143;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase C-like 1 (EC 2.7.1.-) (Protein-kinase C-related kinase
DE 1) (Protein kinase C-like PKN) (Serine-threonine protein kinase N).
GN PRKCL1 OR PRK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95080426; PubMed=7988719;
RA Palmer R.H., Ridden J., Parker P.J.;
RT "Identification of multiple, novel, protein kinase C-related gene
RT products.";
RL FEBS Lett. 356:5-8(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=95154310; PubMed=7851406;
RA Palmer R.H., Ridden J., Parker P.J.;
RT "Cloning and expression patterns of two members of a novel protein-
RT kinase-C-related kinase family.";
RL Eur. J. Biochem. 227:344-351(1995).
RN [3]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-644.
RC TISSUE=Hippocampus;
RX MEDLINE=94183274; PubMed=8135837;
RA Mukai H., Ouo Y.;
RT "A novel protein kinase with leucine zipper-like sequences: its
RT catalytic domain is highly homologous to that of protein kinase C.";
RL Biochem. Biophys. Res. Commun. 199:897-904(1994).
CC -1- FUNCTION: CAN PHOSPHORYLATE RIBOSOMAL PROTEIN S6. MEDIATES GTPASE
CC RHO DEPENDENT INTRACELLULAR SIGNALING (BY SIMILARITY).
CC -1- ENZYME REGULATION: ACTIVATED BY LIPIDS, PARTICULARLY CARDIOLIPIN
CC AND TO A LESSER EXTENT BY OTHER ACIDIC PHOSPHOLIPIDS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- TISSUE SPECIFICITY: FOUND UBQUITOUSLY. EXPRESSED IN HEART, BRAIN,
CC PLACENTA, LUNG, SKELETAL MUSCLE, KIDNEY, AND PANCREAS.
CC -1- PTM: AUTOPHOSPHORYLATED; PREFERABLY IN SERINE.
CC -1- PTM: ACTIVATED BY LIMITED PROTEOLYSIS WITH TRYPSIN (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
CC EMBL; U33053; AAC50209.1; -
CC EMBL; S75546; AAB33345.1; -
CC EMBL; D26181; BAA05169.1; -
CC HSSP; P05132; IATP.
CC Genew; HGNC:9405; PRKCL1.
CC MIM; 601032; -
CC InterPro; IPR000008; C2.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR000961; Pkinase_C.
CC InterPro; IPR000861; REM_repeat.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00433; pkinase_C; 1.
CC Pfam; PF02185; HR1_3.
CC ProDom; PD000001; Euk_pkinase; 1.
CC SMART; SM00239; C2; 1.
CC SMART; SM00074; HR1_3.
CC SMART; SM00133; S_TK_X; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC Transferrase; ATP-binding; Serine/threonine-protein kinase;
CC phosphorylation.
CC DOMAIN 615 874 PROTEIN KINASE.
CC NP_BIND 621 629 ATP (BY SIMILARITY).
CC BINDING 644 644 ATP (BY SIMILARITY).
CC ACT_SITE 740 740 BY SIMILARITY.

```


FT MUTAGEN 644 644 K->R: SUBSTANTIAL REDUCTION OF
FT CONFLICT 191 191 AUTOPHOSPHORYLATION.
SQ SEQUENCE 942 AA; 103989 MW; A89E40DCAEF560E3 CRC64;

Query Match 72.9%; Score 35; DB 1; Length 942;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9

Db 564 QKSSRDPPS 572

RESULT 8

ID URBL_USTMA STANDARD; PRT; 950 AA.
AC P40349;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DE siderophore biosynthesis regulatory protein URBS1.
GN URBS1.
OS Ustilago maydis (Smut fungus).
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=5270;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=518;
RX MEDLINE=94019380; PubMed=8413298;
RA Volzard C.P., Wang J., McEvoy J.L., Xu P., Leong S.A.;
RT "urbs1, a gene regulating siderophore biosynthesis in Ustilago
maydis, encodes a protein similar to the erythroid transcription
factor GATA-1.";
RL Mol. Cell. Biol. 13:7091-7100(1993).

CC -!- FUNCTION: INVOLVED IN THE REGULATION OF SECRETED FERRIC-IRON TYPE
SIDEROPHORES. ACTS DIRECTLY OR INDIRECTLY TO REPRESS THE
BIOSYNTHESIS OF SIDEROPHORES.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: CONTAINS 2 GATA-TYPE ZINC FINGERS.
CC -----

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CC -----

DR EMBL; M80547; AAB05617.1; -.

DR PIR; S27473; S27473.

DR HSP; P17679; LGNF.

DR TRANSFAC; T02406; -.

DR InterPro; IPR000679; Znf_GATA.

DR InterPro; IPR001164; hRIP_Like.

DR Pfam; PF003320; GATA; 2.

DR PRINTS; PR00619; GATAZNFINGER.

DR SMART; SM00401; Znf_GATA; 2.

DR PROSITE; PS00344; GATA_ZN_FINGER_1; 2.

DR PROSITE; PS00114; GATA_ZN_FINGER_2; 2.

KW DNA-binding; Zinc-finger; Transcription regulation; Repressor;

KW Nuclear protein.

FT ZN_FING 338 362 GATA-TYPE 1.

FT ZN_FING 482 506 GATA-TYPE 2.

FT DOMAIN 24 27 POLY-ALA.

FT DOMAIN 28 36 POLY-SER.

FT DOMAIN 487 490 POLY-THR.

FT DOMAIN 753 780 HIS-RICH.

FT DOMAIN 902 906 POLY-SER.

SQ SEQUENCE 950 AA; 101427 MW; F969C6DA09A78C12 CRC64;

Query Match 72.9%; Score 35; DB 1; Length 950;

Best Local Similarity 85.7%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QOSSEDPPT 8

Db 448 QTSSEDPPT 454

RESULT 9

ID KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;

RA Weigert M., Gattmaitan L., Loh E., Schilling J., Hood L.E.;

RT "Rearrangement of genetic information may produce immunoglobulin

diversity.";

RL Nature 276:785-790(1978).

DR PIR; A01937; KVMS43.

DR HSSP; P80362; 1WTL.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGv; 1.

KW immunoglobulin V region.

FT DOMAIN 1 23

FT DOMAIN 24 38

FT DOMAIN 39 53

FT DOMAIN 54 60

FT DOMAIN 61 92

FT DOMAIN 93 101

FT DOMAIN 102 111

FT DISULFID 23 92

FT NON_TER 111 111

SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 111;

Best Local Similarity 77.8%; Pred. No. 7.7;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9

Db 93 QOSNEDPPT 101

RESULT 10

ID KV3O_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;

RA Weigert M., Gattmaitan L., Loh E., Schilling J., Hood L.E.;

RT "Rearrangement of genetic information may produce immunoglobulin

diversity.";

RL Nature 276:785-790(1978).

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DR PIR; C01937; KVM08.
DR HSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

1 QOSSEDPPT 9
111:1111
Db 93 QOSNEDPWT 101

RESULT 11
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity".
RL Nature 276:785-790(1978).
DR PIR; E01937; KVM08.
DR HSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

1 QOSSEDPPT 9
111:1111
Db 93 QOSNEDPWT 101

RESULT 12
VIF_HV2NZ STANDARD; PRT; 215 AA.
ID P05901;
AC P05901;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Virion infectivity factor (SOR protein) (Q protein).
VIF.
GN Human immunodeficiency virus type 2 (isolate NIH-2) (HIV-2).
OS Viruses; Retroviridae; Retroviridae; Lentivirus.
OC NCBI_TaxID=11719;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88320359; PubMed=3261862;
RA Zagury J.F., Franchini G., Reitz M.S. Jr., Collalti E., Starcich B.R.,
RA Hall L., Fargnoli K., Jagodzinski L.L., Guo H.-G., Laure F.,
RA Aya S.K., Josephs S.F., Zagury D., Wong-Staal F., Gallo R.C.;
RT "Genetic variability between isolates of human immunodeficiency virus
RT (HIV) type 2 is comparable to the variability among HIV type 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
CC -----
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CC -----
CC EMBL; J03654; AAB00756.1; -
CC HIV; J03654; VIFs2NIH2.
CC InterPro; IPR000475; Viral_infect.
CC Pfam; PF00559; Vif; 1.
CC PRINTS; PR00349; VIRIONINFECT.
CC ProDom; PD000063; Viral_infect; 1.
CC AIDS.
KW AIDS.
SQ SEQUENCE 215 AA; 25321 MW; 9BA41F36A9690BFC CRC64;

Query Match 70.8%; Score 34; DB 1; Length 215;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
1:11111
Db 192 QRGSESPPT 200

RESULT 13
SPIH_HUMAN STANDARD; PRT; 232 AA.
ID Q99865; O75650; Q9UJU0;
AC Q99865; O75650; Q9UJU0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Spindlin homolog (Protein DXF34).
GN DXF34.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97419273; PubMed=9271673;
RA Laval S.H., Reed V., Blair H.J., Boyd Y.;
RT "The structure of DXF34, a human X-linked sequence family with
RT homology to a transcribed mouse Y-linked repeat.";
RL Mamm. Genome 8:689-691(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Heath P.;
RP Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

```

CC -!- SIMILARITY: BELONGS TO THE SPIN / STSY FAMILY.
CC -----
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CC -----
DR EMBL; Y09858; CAA70988.1; -;
DR EMBL; AL022157; CAA18148.1; -;
DR EMBL; AL022157; CAA18149.1; -;
DR InterPro; IPR003671; Spin_Ssty.
DR Pfam; PF02513; Spin_Ssty; 3.
KW Developmental protein; Phosphorylation; Cell cycle.
FT MOD_RES 196 196 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 224 224 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 20 20 C -> R (IN REF. 2).
FT CONFLICT 208 208 T -> A (IN REF. 2; CAA18149).
SQ SEQUENCE 232 AA; 26536 MW; 093E7B9F5340BF71 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 232;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSSEDPPT 9
: : : : :
Db 165 ESSESPT 172

RESULT 14
GLHR ANTEL
ID GLHR ANTEL STANDARD; PRT; 925 AA.
AC P35409;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable glycoprotein hormone G-protein coupled receptor precursor.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=94107299; PubMed=8280121;
RY Nothacker H.-P.; Grimmelikhuijzen C.J.P.;
RI "Molecular cloning of a novel, putative G protein-coupled receptor
RT LH/CG receptor family from mammals."
RL Biochem. Biophys. Res. Commun. 197;1062-1069(1993).
CC -!- FUNCTION: PROBABLE RECEPTOR FOR A GLYCOPROTEIN HORMONE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC FSH/LSH/TSH SUBFAMILY.
CC -----
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CC -----
DR EMBL; Z28332; CAA82186.1; -;
DR PIR; S41908; S41908.
DR PIR; JC2033; JC2033.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR Pfam; PF00001; 7tm_1; 1.
DR Pfam; PF00560; LRR; 6.

DR SMART; SM00370; LRR; 2.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Alternative splicing; Repeat.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 925 PROBABLE GLYCOPROTEIN HORMONE G-PROTEIN
FT COUPLED RECEPTOR.
FT DOMAIN 28 529 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 530 551 1 (POTENTIAL).
FT DOMAIN 552 561 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 562 584 2 (POTENTIAL).
FT DOMAIN 585 606 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 607 628 3 (POTENTIAL).
FT DOMAIN 629 651 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 652 673 4 (POTENTIAL).
FT DOMAIN 674 691 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 692 712 5 (POTENTIAL).
FT DOMAIN 713 739 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 740 763 6 (POTENTIAL).
FT DOMAIN 764 774 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 775 795 7 (POTENTIAL).
FT DOMAIN 796 925 CYTOPLASMIC (POTENTIAL).
FT REPEAT 333 349 5 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 350 384 1 (INCOMPLETE).
FT REPEAT 385 419 2.
FT REPEAT 420 453 3.
FT REPEAT 454 461 4.
FT CARBOHYD 61 61 5 (INCOMPLETE).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 235 925 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 925 AA; 100059 MW; D03A256368452FBD CRC64;

Query Match 70.8%; Score 34; DB 1; Length 925;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSSEDPPT 9
: : : : :
Db 478 QSTADPPT 485

RESULT 15
P531_HUMAN
ID P531_HUMAN STANDARD; PRT; 1972 AA.
AC Q12888;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor suppressor p53-binding protein 1 (p53-binding protein 1)
DE (53BP1).
GN TP53BP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98421532; PubMed=9748285;
RA Iwabuchi K., Li B., Massa H.F., Trask B.J., Date T., Fields S.;
RT "Stimulation of p53-mediated transcriptional activation by the
RT p53-binding proteins, 53BP1 and 53BP2."
RL J. Biol. Chem. 273:26061-26068(1998).
RN [2]
RN SEQUENCE OF 946-1972 FROM N.A.
RX MEDLINE=94286584; PubMed=8016121;
RA Iwabuchi K., Bartel P.L., Li B., Marraccino R., Fields S.;
RT "Two cellular proteins that bind to wild-type but not mutant p53.";

```
RL  Proc. Natl. Acad. Sci. U.S.A. 91:6098-6102(1994).
CC  -!- FUNCTION: ENHANCES P53-MEDIATED TRANSCRIPTIONAL ACTIVATION.
CC  -!- SUBUNIT: BINDS TO THE CENTRAL DOMAIN OF P53.
CC  -!- SUBCELLULAR LOCATION: NUCLEAR. BOTH NUCLEAR AND CYTOPLASMIC
CC      IN SOME CELLS.
CC  -!- SIMILARITY: CONTAINS 2 BRCT DOMAINS.
CC  -----
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CC  -----
DR  EMBL; AF078776; AAC62018.1; -.
DR  EMBL; U09477; AAA21596.1; -.
DR  Genew; HGNC:11999; TP53BP1.
DR  MIM; 605230; -.
DR  InterPro; IPR001357; BRCT.
DR  Pfam; PF00533; BRCT; 2.
DR  SMART; SM00292; BRCT; 2.
DR  PROSITE; PS01172; BRCT; 2.
DR  Nucleic protein; Transcription regulation; Activator; Repeat.
KW  DOMAIN 1724 1848 BRCT 1.
FT  DOMAIN 1864 1964 BRCT 2.
FT  DOMAIN 1642 1646 POLY-SER.
FT  DOMAIN 1760 1764 POLY-GLU.
SQ  SEQUENCE 1972 AA; 213573 MW; 13E2CC8A265F9D2A CRC64;

Query Match      70.8%; Score 34; DB 1; Length 1972;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 SEDPPT 9
Db  1050 SEDPPT 1055

Search completed: February 14, 2003, 11:16:24
Job time : 5.64516 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model
Run on: February 14, 2003, 11:10:17 ; Search time 18.7258 Seconds
(without alignments)
99.030 Million cell updates/sec

Title: US-09-701-001b-6
Perfect score: 48
Sequence: 1 QOSSEDPPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.rodent:*
- 12: sp.virus:*
- 13: sp.vertebrate:*
- 14: sp.unclassified:*
- 15: sp.rvirus:*
- 16: sp.bacteriaph:*
- 17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	79.2	301	10 Q9SN12	Q9sn12 arabidopsis
2	38	79.2	304	10 Q49745	Q49745 arabidopsis
3	38	79.2	304	10 Q39155	Q39155 arabidopsis
4	38	79.2	564	11 Q9CTV2	Q9ctv2 mus musculus
5	37	77.1	442	10 Q82263	Q82263 arabidopsis
6	35	72.9	265	10 Q8SA13	Q8sal3 oryza sativ
7	35	72.9	231	5 Q8SUS0	Q8sus0 encephalito
8	35	72.9	305	10 Q9FDW1	Q9fdw1 arabidopsis
9	35	72.9	305	10 Q941B3	Q941b3 arabidopsis
10	35	72.9	479	4 Q15523	Q15523 homo sapien
11	35	72.9	874	11 Q99797	Q99797 mus musculus
12	35	72.9	1068	5 Q9W3X2	Q9w3x2 drosophila
13	35	72.9	1113	10 Q9C5K1	Q9c5k1 arabidopsis
14	35	72.9	1116	10 Q9FPT1	Q9fpt1 arabidopsis
15	35	72.9	1126	10 Q9FG10	Q9fg10 arabidopsis
16	35	72.9	1716	11 Q99MS7	Q99ms7 mus musculus

17	34	70.8	96	2	Q9F293	Q9f293 versinia en
18	34	70.8	127	17	Q9HSR1	Q9hsr1 halobacteri
19	34	70.8	227	5	Q9N8Y0	Q9n8y0 trypanosoma
20	34	70.8	258	4	Q9BP22	Q9bp22 homo sapien
21	34	70.8	268	10	Q9SBF6	Q9sbf6 arabidopsis
22	34	70.8	320	10	Q23160	Q23160 arabidopsis
23	34	70.8	333	13	Q9U8W4	Q9u8w4 eptaretus
24	34	70.8	355	16	Q8ZJ49	Q8zj49 versinia pe
25	34	70.8	417	5	Q8T263	Q8t263 dictyosteli
26	34	70.8	452	4	Q9BZ18	Q9bz18 homo sapien
27	34	70.8	476	4	Q9H1J1	Q9h1j1 homo sapien
28	34	70.8	556	10	Q9FFK3	Q9ffk3 arabidopsis
29	34	70.8	652	12	Q85056	Q85056 atkinsonell
30	34	70.8	706	5	Q9SZ15	Q9sz15 caenorhabdi
31	34	70.8	761	5	Q23501	Q23501 caenorhabdi
32	34	70.8	1006	4	Q43150	Q43150 homo sapien
33	34	70.8	1051	11	Q9ESV1	Q9esv1 rattus norv
34	34	70.8	1068	11	Q8R4U7	Q8r4u7 mus musculu
35	34	70.8	1138	5	Q95VA3	Q95va3 drosophila
36	34	70.8	1338	5	Q9VA16	Q9va16 drosophila
37	34	70.8	1543	5	Q9W406	Q9w406 drosophila
38	34	70.8	1608	5	Q95VA5	Q95va5 drosophila
39	34	70.8	1963	5	Q9VSK5	Q9vsk5 drosophila
40	34	70.8	1966	5	Q9NHX6	Q9nhx6 drosophila
41	34	70.8	1985	5	Q8T9N4	Q8t9n4 drosophila
42	34	70.8	2813	4	Q96JP6	Q96jp6 homo sapien
43	34	70.8	2813	4	Q8WXQ6	Q8wxq6 homo sapien
44	34	70.8	2817	4	Q96P79	Q96p79 homo sapien
45	34	70.8	3179	12	Q8V2A4	Q8v2a4 human herpe

ALIGNMENTS

RESULT 1

Q9SN12	ID	Q9SN12	PRELIMINARY;	PRT;	301 AA.
AC	Q9SN12;				
DT	01-MAY-2000	(Tremblrel. 13, Created)			
DT	01-MAY-2000	(Tremblrel. 13, Last sequence update)			
DT	01-MAR-2002	(Tremblrel. 20, Last annotation update)			
DE	R2R3-MYB transcription factor	(AT3g50060/F3A4_140).			
GN	F3A4.140.				
OS	Arabidopsis thaliana	(Mouse-ear cross).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi				
OX	NCBI_TaxID=3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Bargues M., Collado M.C., Navarro P., Terol J., Perez-Alonso M.,				
RA	Newes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;				
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	EU Arabidopsis sequencing project;				
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,				
RA	Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,				
RA	Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,				
RA	Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,				
RA	Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,				
RA	Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,				
RA	Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,				
ET	Ecker J.R.;				
RL	"Arabidopsis cDNA clones";				
CC	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.				
CC	-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).				
DR	EMBL; AL132978; CAB62114.1; -				
DR	EMBL; AF424588; AAL11582.1; -				

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DR HSSP; P01103; IPOM.
DR InterPro; IPR001005; Myb_DNA_binding.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00334; MYB_2; UNKNOWN_2.
DR PROSITE; PS00090; MYB_3; 2.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 301 AA; 33111 MW; 9CCD5863E9D06DEC CRC64;

Query Match          79.2%; Score 38; DB 10; Length 301;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SSEDPT 9
Db 197 SSEDPT 203

RESULT 2
O49745 PRELIMINARY; PRT; 304 AA.
O49745;
01-JUN-1998 (TREMBLrel. 06, Created)
01-JUN-1998 (TREMBLrel. 06, Last sequence update)
01-MAR-2002 (TREMBLrel. 20, Last annotation update)
R2R3-MYB transcription factor.
GN ATWB77.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RA Romero I., Fuentes A., Benito M.J., Malpica J., Leyva A., Paz-Ares J.;
RT "One hundred R2R3-MYB genes in the genome of Arabidopsis thaliana.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
DR EMBL; Y14208; CAA74604.1; -.
DR EMBL; Y14208; CAA74604.1; -.
DR HSSP; P01103; IPOM.
DR InterPro; IPR001005; Myb_DNA_binding.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00334; MYB_2; UNKNOWN_2.
DR PROSITE; PS00090; MYB_3; 2.
KW DNA-binding; Nuclear protein.
VARIANT 136 136 S -> P.
VARIANT 298 298 I -> V.
SQ SEQUENCE 304 AA; 33296 MW; 53AE63F19CC24B42 CRC64;

Query Match          79.2%; Score 38; DB 10; Length 304;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SSEDPT 9
Db 197 SSEDPT 203

RESULT 3
Q39155 PRELIMINARY; PRT; 304 AA.
Q39155;
01-NOV-1996 (TREMBLrel. 01, Created)
01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE MYB-related protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=LANDSBERG ERECTA; TISSUE=SILTIQUES;
RX MEDLINE=98341717; PubMed=9678577;
RA Kirik V., Kolbe K., Misera S., Baumelein H.;
RT "Two novel MYB homologues with changed expression in late
RT embryogenesis-defective Arabidopsids mutants.";
RL plant Mol. Biol. 37:819-827(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
DR EMBL; Z54137; CAA90810.1; -.
DR HSSP; P01103; IPOM.
DR TRANSFAC; T02590; -.
DR InterPro; IPR001005; Myb_DNA_binding.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00334; MYB_2; UNKNOWN_2.
DR PROSITE; PS00090; MYB_3; 2.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 304 AA; 33292 MW; EFA25289C3FD5A21 CRC64;

Query Match          79.2%; Score 38; DB 10; Length 304;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SSEDPT 9
Db 197 SSEDPT 203

RESULT 4
Q9CTV2 PRELIMINARY; PRT; 564 AA.
Q9CTV2;
01-JUN-2001 (TREMBLrel. 17, Created)
01-JUN-2001 (TREMBLrel. 17, Last sequence update)
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 4933434L15RIK protein (Fragment).
GN 4933434L15RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=THYMUS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK020021; BAB31969.1; -.
DR MGD; MGI:1914803; 4933434L15RIK.
DR InterPro; IPR004046; GST_Cterm.

```

DR InterPro: IPR000051; SAM_bind.

DR Pfam: PF0043; GST_C; 1.

FT NON_TER 1

SQ SEQUENCE 564 AA; 62710 MW; 8EAF7A27E35B53DA CRC64;

Query Match 79.2%; Score 38; DB 11; Length 564;

Best Local Similarity 77.8%; Pred. No. 19;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9

1:|||||

Db 94 QESSEHPPT 102

RESULT 5

O82263 PRELIMINARY; PRT; 442 AA.

ID O82263

O82263; Q944K4;

01-NOV-1998 (TrEMBLrel. 08, Created)

01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Expressed protein (A2947960/T923.10) (Hypothetical 49.3 kDa

protein).

GN AT2947960.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;

OC Eurosid II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLOMBIA;

RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,

RA Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLOMBIA;

RA Lin X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLOMBIA;

RA Town C.D., Kaul S.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLOMBIA;

RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,

RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,

RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,

RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,

RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,

RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,

RA Ecker J.R.;

RT "Arabidopsis cDNA clones";

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,

RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,

RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,

RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,

RA Davis R.W., Ecker J.R., Theologis A.;

RT "Full length cDNA of gene At2g47960 (GI:15227177).";

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLOMBIA;

RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,

RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,

RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,

RA Fraser C.M., Venter J.C.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC005309; AAC63650.2; -;

DR EMBL; AF428334; AAL16264.1; -;

DR EMBL; AY074352; AAL67048.1; -;

DR EMBL; AC006072; AAM15133.1; -;

KW Hypothetical protein

SQ SEQUENCE 442 AA; 49290 MW; D6E987FA3D95BE30 CRC64;

Query Match 77.1%; Score 37; DB 10; Length 442;

Best Local Similarity 66.7%; Pred. No. 24;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9

1:|||||

Db 246 EDSTEDPPT 254

RESULT 6

Q8SA13

PRELIMINARY; PRT; 265 AA.

ID Q8SA13

Q8SA13;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE P0703B11.5 protein.

GN P0703B11.5.

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. NIPPONBARE;

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC

clone:P0703B11.5";

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP003302; BAB85286.1; -;

SQ SEQUENCE 265 AA; 29807 MW; C779784F75C06E7F CRC64;

Query Match 72.9%; Score 35; DB 10; Length 265;

Best Local Similarity 75.0%; Pred. No. 36;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 8

1:|||||

Db 93 QHNSDDPP 100

RESULT 7

Q8SUS0

PRELIMINARY; PRT; 291 AA.

ID Q8SUS0

Q8SUS0;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Hypothetical protein EC008_0540.

GN EC008_0540.

OS Encephalitozoon cuniculi.

OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.

OX NCBI_TaxID=6035;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GB-M1;

RA Genoscope;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=GB-M1;

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RX MEDLINE-21576510; PubMed-11719806;
RA Katinka M.B., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL; AL590448; CAD26359.1; -.
KW Hypothetical protein.
SQ SEQUENCE 291 AA; 31902 MW; 70ABBB450CD45D35 CRC64;

Query Match 72.9%; Score 35; DB 5; Length 291;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 8
Db 268 QNASDEPPT 275
ID Q9FDW1 PRELIMINARY; PRT; 305 AA.
AC Q9FDW1
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative myb-related protein (Myb-related protein, 33.3K).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eusoids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Etgu P., Lee J.M.,
RA Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full Length cDNA of gene K8K14.2 (GI:9758429).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE-98162728; PubMed-9501997;
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asanizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT Sequence features of the regions of 1,191,918 bp covered by seventeen
RT physically assigned pl clones.";
RL DNA Res. 4:401-414(1997).
[3]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Theologis A.;
RT "Full Length cDNA of gene K8K14.2 (GI:9758429).";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SURCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
DR EMBL; AF326877; AAG41459.1; -.
DR EMBL; AB007645; BAB09015.1; -.
DR EMBL; AF339698; AAK00380.1; -.
DR HSP; P01103; 1POM.
DR InterPro; IPR001005; Myb_DNA_binding.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00334; MYB_2; UNKNOWN_2.

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DR PROSITE; PS50090; MYB_3; 2.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 305 AA; 33268 MW; FDD31F9916E14D9D CRC64;

Query Match 72.9%; Score 35; DB 10; Length 305;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SSEDPPPT 9
Db 186 SDDPPT 192
ID Q941B3 PRELIMINARY; PRT; 305 AA.
AC Q941B3
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE AT5g67300/K8K14.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eusoids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY052297; AAK96490.1; -.
DR EMBL; AY061923; AAL31250.1; -.
DR InterPro; IPR001005; Myb_DNA_binding.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; UNKNOWN_2.
DR PROSITE; PS50090; MYB_3; 2.
SQ SEQUENCE 305 AA; 33282 MW; FDD31F990BDBE4F CRC64;

Query Match 72.9%; Score 35; DB 10; Length 305;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SSEDPPPT 9
Db 186 SDDPPT 192
ID Q15523 PRELIMINARY; PRT; 479 AA.
AC Q15523
DT 01-NOV-1996 (TREMBLrel. 01, Created)

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DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-WAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Serine/threonine protein kinase.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95045520; PubMed=7957185;
 RA Chu W., Presky D.H., Danho W., Swerlick R.A., Burns D.K.;
 RT "Identification and characterization of DBK, a novel putative
 RT serine/threonine protein kinase from human endothelial cells.";
 RL Eur. J. Biochem. 225:695-702(1994).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; X80229; CAA56515.1; -;
 DR HSSP; P05132; IATP.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000961; Kinase_C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TK; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 479 AA; 53005 MW; 1ADF5B548828485 CRC64;

Query Match 72.9%; Score 35; DB 4; Length 479;
 Best Local Similarity 66.7%; Pred. No. 66;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
 :||| |||
 DB 101 QKSSRDPPS 109

RESULT 11
 Q99J97 PRELIMINARY; PRT; 874 AA.
 ID AC Q99J97
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Tangerin B (Similar to KIAA0903 protein).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BALE/C;
 RA Melichar J.M., Noegel A.A., Korenbaum E.;
 RT "Tangerin, a novel Golgi-associated protein with calponin-homology
 RT domain and CAAX-box".
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF305088; AAK32110.1; -;
 DR EMBL; BC004660; AAH04660.1; -;
 DR HSSP; Q01082; IAKR.
 DR InterPro; IPR001715; Calponin-like.
 DR InterPro; IPR001230; Prenyl_site.
 DR Pfam; PF00307; CH; 1.
 DR SMART; SM00033; CH; 1.
 DR PROSITE; PS00021; CH; 1.
 DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
 SQ SEQUENCE 874 AA; 95560 MW; 94803958BCDF5B6D CRC64;

Query Match 72.9%; Score 35; DB 11; Length 874;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SSEDPT 9
 :||| |||
 DB 327 TSEDPT 333
 RESULT 12
 Q9W3X2 PRELIMINARY; PRT; 1068 AA.
 ID AC Q9W3X2
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE CG14442 protein.
 GN CG14442.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003438; AAF46190.1; -;
 DR FlyBase; FBgn0029893; CG14442.
 DR InterPro; IPR000425; MIP_family.
 DR PROSITE; PS00221; MIP; UNKNOWN_1.
 SQ SEQUENCE 1068 AA; 118348 MW; 9E50BDCDD343995B CRC64;

Query Match 72.9%; Score 35; DB 5; Length 1068;

Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
Db 114 QOSQPPPT 122

RESULT 13

Q9C5K1 PRELIMINARY; PRT; 1115 AA.
AC Q9C5K1; (TREMREL. 17, Created)
DT 01-JUN-2001 (TREMREL. 17, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Putative ubiquitin carboxyl-terminal hydrolase.
GN F15M7.13/AT5G06600.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;

[1]

SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene F15M7.13/AT5G06600 (GI:10178116).";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF360198; AAK25908.1; -
DR InterPro: IPR002083; MATH.
DR InterPro: IPR001448; SASP.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00917; MATH; 1.
DR Pfam: PF00240; ubiquitin; 1.
DR Pfam: PF00442; UCH-1; 1.
DR Pfam: PF00443; UCH-2; 1.
DR SMART: SM00061; MATH; 1.
DR PROSITE: PS00304; SASP_1; UNKNOWN_1.
DR PROSITE: PS00972; UCH_2_1; 1.
DR PROSITE: PS00973; UCH_2_2; 1.
DR PROSITE: PS0235; UCH_2_3; 1.
KW Hydrolase.

QY 2 QOSSEDPPT 9

Db 46 QPAEDPPT 53

RESULT 14

Q9FPF1 PRELIMINARY; PRT; 1116 AA.
AC Q9FPF1; (TREMREL. 16, Created)
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Ubiquitin-specific protease 12.
GN UB12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;

QY 2 QOSSEDPPT 9
Db 46 QPAEDPPT 53

RESULT 15

Q9FG10 PRELIMINARY; PRT; 1126 AA.
AC Q9FG10; (TREMREL. 16, Created)
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;

SEQUENCE FROM N.A.
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP002543; BAB11409.1; -
DR InterPro: IPR002083; MATH.
DR InterPro: IPR001448; SASP.
DR InterPro: IPR000626; Ubiquitin.
DR InterPro: IPR001394; UCH-2.
DR Pfam: PF00917; MATH; 1.
DR Pfam: PF00240; ubiquitin; 1.
DR Pfam: PF00442; UCH-1; 1.
DR Pfam: PF00443; UCH-2; 1.
DR SMART: SM00061; MATH; 1.
DR PROSITE: PS00304; SASP_1; UNKNOWN_1.
DR PROSITE: PS00972; UCH_2_1; 1.
DR PROSITE: PS00973; UCH_2_2; 1.
DR PROSITE: PS0235; UCH_2_3; 1.
KW Hydrolase.

QY 2 QOSSEDPPT 9

Db 47 QPAEDPPT 54

RESULT 16

Q9FG10 PRELIMINARY; PRT; 1126 AA.
AC Q9FG10; (TREMREL. 16, Created)
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;

QY 2 QOSSEDPPT 9

Db 47 QPAEDPPT 54

us-09-701-001b-6.rspt

Fri Feb 14 15:01:00 2003

Qy 2 QSSDPPT 9
| :|||||
Db 56 QPAEDPPT 63

Search completed: February 14, 2003, 11:18:45
Job time : 20.8925 secs

